

OM protein - protein search, using sw model

Run on: February 25, 2004, 16:12:26 ; Search time 60 Seconds  
 (without alignments)  
 1492.793 Million cell updates/sec

Title: US-09-787-126-2  
 Perfect score: 1685  
 Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1685	100.0	317	2	AAW83195	Aaw83195 Human ost
2	1685	100.0	317	2	AAW69957	Aaw69957 NF-kB rec
3	1685	100.0	317	2	AAW68293	Aaw68293 NF-kB rec
4	1685	100.0	317	2	AAE08738	Aae08738 Human rec
5	1685	100.0	317	3	AAY84417	Aay84417 Amino aci
6	1685	100.0	317	4	AAE04426	Aae04426 Human rec
7	1685	100.0	317	4	AAE01993	Aae01993 Human ful
8	1685	100.0	317	5	ABB08134	Abb08134 Human RAN
9	1685	100.0	317	5	AAE26103	Aae26103 Human RAN

10	1685	100.0	317	5	ABG31631	Abg31631 Human RAN
11	1685	100.0	317	5	AAU78285	Aau78285 Human TRA
12	1685	100.0	317	5	AAO19096	Aao19096 C neoform
13	1685	100.0	317	6	ABP55108	Abp55108 Human ost
14	1685	100.0	317	6	AAE34364	Aae34364 Human rec
15	1685	100.0	317	6	ABR42314	Abr42314 Human RAN
16	1685	100.0	317	7	ADB16988	Adb16988 Human rec
17	1685	100.0	317	7	ADC35204	Adc35204 Human TNF
18	1685	100.0	317	7	ADC73002	Adc73002 Human RAN
19	1685	100.0	317	7	ADC78268	Adc78268 Human RAN
20	1677	99.5	317	2	AAW83018	Aaw83018 Osteoclas
21	1417.5	84.1	316	2	AAW83017	Aaw83017 Osteoclas
22	1417.5	84.1	316	2	AAW83194	Aaw83194 Human ost
23	1417.5	84.1	316	2	AAW59654	Aaw59654 Amino aci
24	1417.5	84.1	316	2	AAY17874	Aay17874 Murine TR
25	1417.5	84.1	316	3	AAY91024	Aay91024 Mouse OBM
26	1417.5	84.1	316	3	AAY84418	Aay84418 Amino aci
27	1417.5	84.1	316	3	AAY84419	Aay84419 Amino aci
28	1417.5	84.1	316	5	AAU78289	Aau78289 Mouse TRA
29	1417.5	84.1	316	6	ABR42071	Abr42071 Human RAN
30	1417.5	84.1	316	6	ABB99477	Abb99477 Amino aci
31	1417.5	84.1	316	6	ABU08463	Abu08463 Amino aci
32	1417.5	84.1	316	6	ABR55560	Abr55560 Amino aci
33	1396.5	82.9	318	4	AAB82092	Aab82092 Rat osteo
34	1326.5	78.7	294	2	AAW69956	Aaw69956 NF-kB rec
35	1326.5	78.7	294	2	AAW68292	Aaw68292 NF-kB rec
36	1326.5	78.7	294	2	AAE08737	Aae08737 Murine re
37	1326.5	78.7	294	4	AAE04425	Aae04425 Murine re
38	1326.5	78.7	294	4	AAE01992	Aae01992 Murine RA
39	1326.5	78.7	294	5	AAE26102	Aae26102 Mouse RAN
40	1326.5	78.7	294	7	ADB16986	Adb16986 Murine re
41	1326.5	78.7	294	7	ADC73000	Adc73000 Murine RA
42	1326.5	78.7	294	7	ADC78266	Adc78266 Murine RA
43	1325	78.6	250	6	ADA50079	Ada50079 Human wil
44	1322	78.5	250	6	ADA50095	Ada50095 Human RAN
45	1322	78.5	250	6	ADA50094	Ada50094 Human RAN

# ALIGNMENTS

## RESULT 1

AAW83195

ID AAW83195 standard; protein; 317 AA.

XX

AC AAW83195;

XX

DT 11-FEB-1999 (first entry)

XX

DE Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.1insert.

XX

KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;  
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;  
 KW hypercalcaemia; osteoclast differentiation and activation receptor;  
 KW Paget's disease.

XX

OS Homo sapiens.



QY 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 |||  
 QY 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
 |||  
 QY 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 2

AAW69957

ID AAW69957 standard; protein; 317 AA.  
 XX  
 AC AAW69957;  
 XX  
 DT 08-OCT-1998 (first entry)  
 XX  
 DE NF-kB receptor activator RANK ligand (RANKL).  
 XX  
 KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
 KW immune response; inflammatory response; toxic shock; sepsis; RANKL;  
 KW RANK ligand; tumour necrosis factor; TNF.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09828426-A2.  
 XX  
 PD 02-JUL-1998.  
 XX  
 PF 22-DEC-1997; 97WO-US023775.  
 XX  
 PR 23-DEC-1996; 96US-0059978P.  
 PR 07-MAR-1997; 97US-00813509.  
 PR 14-OCT-1997; 97US-0064671P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Galibert LJ, Maraskovsky E;  
 XX  
 DR WPI; 1998-377657/32.  
 DR N-PSDB; AAV41378.  
 XX  
 PT New isolated ligand for receptor activator of NF-kappa B - used to  
 PT develop products for augmenting an immune response for inhibiting an  
 PT inflammatory response and for protection of cells.  
 XX  
 PS Claim 27; Page 59-60; 80pp; English.  
 XX

CC This represents a human RANKL, a ligand for the RANK (receptor activator  
 CC of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the  
 CC tumour necrosis factor (TNF) family. A soluble RANK may be used for  
 CC inhibiting activation of NF-kB, by contacting a cell expressing membrane-  
 CC associated RANK with a soluble RANK which binds to RANK ligand (RANKL).  
 CC RANKL polypeptides can activate RANK and can be used to induce maturation  
 CC of dendritic cells and enhance their allo-stimulatory capacity, thereby  
 CC augmenting an immune response. The soluble RANK polypeptide composition  
 CC may also be used for regulating an immune or inflammatory response.  
 CC Inhibition of NF-kB by RANK antagonists may be useful in ameliorating  
 CC negative effects of an inflammatory response that result from triggering  
 CC of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host  
 CC reactions, or acute inflammatory reactions. They can also be used in  
 CC adjunct therapy for disease characterised by neoplastic cells that  
 CC express RANK. RANKL polypeptides can also be used to identify inhibitors  
 CC of RANK and thus inhibitors of an inflammatory response, and also for  
 CC protecting RANK-expressing cells from the negative effects of  
 CC chemotherapy or the presence of high levels of TNF-alpha. The products  
 CC can also be used for detection and drug screening

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 3

AAW68293

ID AAW68293 standard; protein; 317 AA.

XX

AC AAW68293;

XX



Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 QY 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 QY 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 QY 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
 QY 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 4

AAE08738

ID AAE08738 standard; protein; 317 AA.

XX

AC AAE08738;

XX

DT 15-NOV-2001 (first entry)

XX

DE Human receptor activator of NF kappaB ligand (RANKL) protein.

XX

KW Human; receptor activator of nuclear factor kappaB ligand; RANKL; NF;

KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;

KW immune response; inflammatory response; graft-versus-host reaction;

KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;

KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX

OS Homo sapiens.

XX

PN US6271349-B1.

XX

PD 07-AUG-2001.

XX

PF 17-DEC-1998; 98US-00215649.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 23-DEC-1996; 96US-00772330.

PR 07-MAR-1997; 97US-0077181P.

PR 07-MAR-1997; 97US-00813509.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Dougall WC, Galibert L;

XX  
DR WPI; 1998-377655/32.  
DR N-PSDB; AAD15311.  
XX  
PT New isolated receptor activator of necrosis factor-kappa B - useful for,  
PT e.g. developing products for regulating an immune or inflammatory  
PT response, treating toxic shock or sepsis.  
XX  
PS Example 15; Col 71-72; 47pp; English.  
XX  
CC The patent discloses novel receptor activator of nuclear factor (NF)-  
CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of  
CC the tumour necrosis factor (TNF) receptor superfamily and associates with  
CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the  
CC regulation of immune and inflammatory response. The receptors are useful  
CC for regulating immune response and in screening for inhibitors of these  
CC receptors. The cytoplasmic domain of RANK is used in developing assays  
CC for inhibitors of signal transduction, e.g. for screening the molecules  
CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and  
CC particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful  
CC in ameliorating the negative effects of an inflammatory response that  
CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,  
CC graft-versus-host reactions, acute inflammatory reactions and the effects  
CC of bone resorption. RANK acts as an anti- apoptotic signal and rescue the  
CC cells that express RANK from apoptosis. Soluble forms of the receptor are  
CC used in vivo or in vitro based screening tests for agonists or  
CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B  
CC activation, or to inhibit transduction of a signal via RANK. RANK  
CC compositions are used in the development of both agonistic and  
CC antagonistic antibodies, or as an adjunct therapy for disease  
CC characterised by neoplastic cells that express RANK. Compounds that  
CC interfere with RANK/TRAF6 interactions are useful for modulating the  
CC formation of osteoclasts from osteoclast precursors and for modulating  
CC osteoclast function and activities. They are used as inhibitors of  
CC diseases associated with excess bone resorption and as immunosuppressants  
CC or anti-inflammatory agents. The RANK DNAs are useful for the expression  
CC of recombinant proteins, as probes for analysis of the presence or  
CC distribution of RANK transcripts, while the proteins are useful in  
CC preparing kits for the detection of soluble RANK, or monitor RANK-related  
CC activity. The present sequence is RANK ligand (RANKL) protein from human  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 2; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
|  
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
|  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
|



Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEA QPF AHLTINATDIPSGSH 180

QY 181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||

Db 181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300  
 |||

Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

QY 301 PDQDATYFGAFKVRDID 317  
 |||

Db 301 PDQDATYFGAFKVRDID 317

RESULT 5

AA Y84417

ID AAY84417 standard; protein; 317 AA.

XX

AC AAY84417;

XX

DT 25-JUL-2000 (first entry)

XX

DE Amino acid sequence of a human osteoprotegerin ligand (OPGL).

XX

KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;

KW tumour necrosis factor receptor; type II transmembrane protein;

KW osteoclast differentiation; CSF-1; osteoclast activator; immune response;

KW osteoporosis; bone resorption.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 49. .69

FT /note= "transmembrane region"

FT Domain 70. .157

FT /note= "extracellular stalk domain"

FT Region 158. .317

FT /note= "active ligand moiety"

XX

PN WO200015807-A1.

XX

PD 23-MAR-2000.

XX

PF 13-SEP-1999; 99WO-DK000481.

XX

PR 15-SEP-1998; 98DK-00001164.

PR 02-OCT-1998; 98US-0102896P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Halkier T, Haaning J;

XX

DR WPI; 2000-271444/23.

DR N-PSDB; AAZ99964.

XX

PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to

PT treat, prevent and ameliorate osteoporosis.  
 XX  
 PS Claim 19; Page 78-79; 110pp; English.  
 XX  
 CC The present sequence represents a human osteoprotegerin ligand (OPGL).  
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor  
 CC receptor family, which blocks osteoclastogenesis in a dose dependent  
 CC manner. The OPGL protein is synthesised as a type II transmembrane  
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL  
 CC is a potent osteoclast differentiation factor when combined with CSF-1.  
 CC It is not capable of inducing osteoclast differentiation in the absence  
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The  
 CC specification describes a method for the in vivo down-regulation of OPGL  
 CC activity in an animal. The method comprises using at least one OPGL  
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce  
 CC an immune response in the animal. The method and OPGL polypeptide are  
 CC useful for treating, preventing and ameliorating osteoporosis or other  
 CC diseases or conditions characterised by excessive bone resorption  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 3; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 Qy 181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLS SWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240  
 Qy 241 YVTKT SIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKT SIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 Qy 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 6  
 AAE04426  
 ID AAE04426 standard; protein; 317 AA.  
 XX  
 AC AAE04426;  
 XX  
 DT 04-SEP-2001 (first entry)



Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 7

AAE01993

ID AAE01993 standard; protein; 317 AA.

XX

AC AAE01993;

XX

DT 31-JUL-2001 (first entry)

XX

DE Human full-length RANKL (receptor activator of NF-kappaB ligand).

XX

KW Human; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;  
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;  
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;  
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;  
 KW immune system dysfunction; familial expansile osteolysis; FEO;  
 KW early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.

XX

OS Homo sapiens.

XX

PN WO200136637-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-US031459.

XX

PR 17-NOV-1999; 99US-00442029.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Anderson DM, Hughes AE;

XX

DR WPI; 2001-329222/34.

DR

N-PSDB; AAD05904.

XX

PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the  
 PT treatment of Pagets disease and Familial Expansile Osteolysis (FEO).

XX

PS Disclosure; Page 76-77; 96pp; English.

XX

CC The present invention relates to a novel receptor, referred to as RANK  
CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF  
CC (tumour necrosis factor) receptor superfamily. RANK is a Type I  
CC transmembrane protein that interacts with TNF receptor-associated factors  
CC (TRAFs). Triggering of RANK by overexpression or co-expression of RANK  
CC and membrane bound RANK ligand (RANKL) results in upregulation of the  
CC transcription factor NF-kappaB, a ubiquitous transcription factor that is  
CC most extensively utilised in cells of the immune system. Inhibition of NF  
CC -kappaB by RANK antagonists is useful in ameliorating negative effects of  
CC inflammatory reactions, and the effects of excess bone resorption. The  
CC RANK DNAs, proteins and their analogues are useful for the preparation of  
CC pharmaceutical compositions, for infecting target cells for use in gene  
CC therapy applications in diagnosing diseases associated with RANK, and as  
CC targets for use in screening assays. They may be used in the treatment or  
CC diagnosis of immune system dysfunction. The present invention also  
CC encompasses gene therapy methods to correct gene-activating mutations,  
CC associated with e.g. familial expansile osteolysis (FEO) and early onset  
CC Paget's disease of bone (EP). The present amino acid sequence is full-  
CC length human RANKL (huRANKL) protein. The RANKL gene is located in  
CC chromosome 13q14

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
|  
Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
|  
Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
Qy 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
|  
Db 121 QAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
  
Qy 181 KVSLSWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240  
|  
Db 181 KVSLSWYH DRGWAKISNM TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEY LQLMV 240  
  
Qy 241 YVTKT SIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
|  
Db 241 YVTKT SIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
  
Qy 301 PDQDATYFGAFKVRDID 317  
|  
Db 301 PDQDATYFGAFKVRDID 317

RESULT 8  
ABB08134

ID ABB08134 standard; protein; 317 AA.  
 XX  
 AC ABB08134;  
 XX  
 DT 10-SEP-2002 (first entry)  
 XX  
 DE Human RANKL polypeptide.  
 XX  
 KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;  
 KW fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;  
 KW tuberculostatic; cytostatic; human; RANKL.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200236141-A2.  
 XX  
 PD 10-MAY-2002.  
 XX  
 PF 30-OCT-2001; 2001WO-US044834.  
 XX  
 PR 02-NOV-2000; 2000US-0245721P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;  
 PI Thomas EK;  
 XX  
 DR WPI; 2002-500114/53.  
 XX  
 PT Treating an individual suffering from infection, e.g. inflammation,  
 PT chickenpox or AIDS, by administering a combination of dendritic cell  
 PT mobilization factor or maturation agent, T cell enhancing factor and  
 PT antigen-specific T cells.  
 XX  
 PS Disclosure; Page 42-43; 43pp; English.  
 XX  
 CC The invention relates to treating an individual at risk for or suffering  
 CC from infection with a pathogenic or opportunistic organism. The method  
 CC involves administering a combination of two to five agents comprising:  
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation  
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;  
 CC or (e) activated, antigen-specific T cells. The methods are useful for  
 CC treating an individual at risk for or suffering from infection with a  
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria  
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.  
 CC T. cruzi, which causes Chaga's disease). The methods are especially  
 CC useful for treating an individual suffering from immunosuppression by  
 CC enhancing a lymphocyte-mediated immune response. In particular, the  
 CC method is useful for treating inflammations, chickenpox, oral or genital  
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T  
 CC cell leukemia or T cell lymphoma. The activated antigen-presenting  
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence  
 CC represents a human RANKL polypeptide fragment  
 XX  
 SQ Sequence 317 AA;

Query Match

100.0%; Score 1685; DB 5; Length 317;

Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
      |||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120
      |||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
      |||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
      |||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300
      |||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
      |||||||
Db    301 PDQDATYFGAFKVRDID 317

```

# RESULT 9

AAE26103

ID AAE26103 standard; protein; 317 AA.

XX

AC AAE26103;

XX

DT 14-NOV-2002 (first entry)

XX

DE Human RANK ligand (RANKL) protein.

XX

KW Human; RANK; receptor activator of nuclear factor-kappaB; NF-kB; sepsis;  
KW immune response; toxic shock; graft-versus-host reaction; therapy; TRAF;  
KW tumour necrosis factor receptor-associated factor; immunosuppressive;  
KW antibacterial; antiinflammatory; chromosome 13.

XX

OS Homo sapiens.

XX

PN US2002086827-A1.

XX

PD 04-JUL-2002.

XX

PF 30-MAY-2001; 2001US-00871291.

XX

PR 23-DEC-1996; 96US-0059978P.

PR 07-MAR-1997; 97US-0077181P.

PR 14-OCT-1997; 97US-0064671P.

PR 22-DEC-1997; 97US-00996139.

PR 17-DEC-1999; 99US-00466496.

PR 24-MAY-2000; 2000US-00577800.





Qy 301 PDQDATYFGAFKVRDID 317  
          |||||  
Db 301 PDQDATYFGAFKVRDID 317

RESULT 10

ABG31631

ID ABG31631 standard; protein; 317 AA.

XX

AC ABG31631;

XX

DT 29-NOV-2002 (first entry)

XX

DE Human RANKL protein.

XX

KW Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;  
KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;  
KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;  
KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;  
KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;  
KW dendritic cell activator; T cell enhancer; human; RANKL.

XX

OS Homo sapiens.

XX

PN WO200266044-A2.

XX

PD 29-AUG-2002.

XX

PF 23-OCT-2001; 2001WO-US046254.

XX

PR 24-OCT-2000; 2000US-0242868P.

XX

PA (IMMV ) IMMUNEX CORP.

XX

PI Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;

XX

DR WPI; 2002-674891/72.

XX

PT Treating an individual with tumors or cancers, e.g. liver cancer or brain  
PT tumor, by administering a combination of dendritic cell populations, T  
PT cell enhancing factors and activated, antigen-specific T cells.

XX

PS Disclosure; Page 43-44; 44pp; English.

XX

CC The present invention relates to a new method for treating a tumour-  
CC bearing subject. The method involves administering a combination of 2 to  
CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell  
CC maturation agent, tumour-killing agent, T cell enhancing factor or  
CC activated, antigen-specific T cells. The method is useful for treating  
CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver  
CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or  
CC cervical intraepithelial neoplasia. The present amino acid sequence  
CC represents the human RANKL protein that was used in the method of the  
CC invention

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 5; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
      ||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317
  
```

RESULT 11

AAU78285

ID AAU78285 standard; protein; 317 AA.

XX

AC AAU78285;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human TRANCE protein splice variant 1.

XX

KW Human; tumour necrosis factor-related activation induced cytokine;  
 KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;  
 KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;  
 KW rheumatoid arthritis; acromegaly; gigantism; exostosis; carilaginea;  
 KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;  
 KW cartilage growth; skeletal growth.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 126. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 137. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 140. .317

FT /note= "Specifically claimed in claims 17 and 18"

FT Region 145. .317

FT /note= "Specifically claimed in claims 17 and 18"

```

FT      Region          158. .317
FT                               /note= "Specifically claimed in claims 17 and 18"
FT      Domain          159. .317
FT                               /note= "TNF core domain, specifically claimed in claims
FT                               17 and 18"
XX
PN      WO200216551-A2.
XX
PD      28-FEB-2002.
XX
PF      20-AUG-2001; 2001WO-US026101.
XX
PR      18-AUG-2000; 2000US-0226197P.
XX
PA      (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
PI      Choi Y,  Odgren PR,  Marks SC;
XX
DR      WPI; 2002-304119/34.
DR      N-PSDB; ABK12876.
XX
PT      Treating mammal having disorder characterized by abnormal
PT      cartilage/skeletal growth such as dwarfism, acromegaly, by administering
PT      tumor necrosis factor-related activation induced cytokine-modulating
PT      agent to mammal.
XX
PS      Disclosure; Fig 10; 55pp; English.
XX
CC      The present invention relates to a new method of treating a mammal having
CC      a disorder comprising insufficient or excessive cartilage or skeletal
CC      growth. The method of the invention involves administering to the mammal
CC      a tumour necrosis factor-related activation induced cytokine (TRANCE)-
CC      modulating agent. The method is useful for treating a mammal having a
CC      disorder comprising insufficient or excessive cartilage or skeletal
CC      growth, where the disorder comprising insufficient cartilage or skeletal
CC      growth is selected from dwarfism, osteopetrosis, craniofacial-skeletal
CC      discrepancies and bone or cartilage damage resulting from traumatic
CC      injury, surgery, osteoarthritis or rheumatoid arthritis, and disorders
CC      comprising excessive cartilage or skeletal growth are selected from
CC      acromegaly, gigantism, exostosis, carilaginea, exostosis bursata and
CC      multiple osteocartilaginous exostoses. The method is useful for
CC      inhibiting chondrocyte differentiation. The present amino acid sequence
CC      represents the human TRANCE protein, splice variant 1, of the invention.
CC      TRANCE is a member of the tumour necrosis factor family and acts directly
CC      on cartilage-producing cells (chondrocytes)
XX
SQ      Sequence 317 AA;

Query Match          100.0%;  Score 1685;  DB 5;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 4.3e-154;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
      |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy      61 VCSVALFFYFRAQMDPNRI SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

```

Db	61	VCSVALFFYFRAQMDPNRISEDGTHCTYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 12

AAO19096

ID AAO19096 standard; protein; 317 AA.  
 XX  
 AC AAO19096;  
 XX  
 DT 22-NOV-2002 (first entry)  
 XX  
 DE C neoformans antigen expressing dendritic cell related protein #5.  
 XX  
 KW Human; fungicide; fungal infection; dendritic cell; antigen;  
 KW Cryptococcus neoformans; vaccine; immunostimulant.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200266053-A2.  
 XX  
 PD 29-AUG-2002.  
 XX  
 PF 14-DEC-2001; 2001WO-US048288.  
 XX  
 PR 04-JAN-2001; 2001US-0259653P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Thomas EK;  
 XX  
 DR WPI; 2002-674896/72.  
 XX  
 PT Producing a population of activated, Cryptococcus neoformans antigen-  
 PT presenting dendritic cells for preventing or treating C. neoformans  
 PT infection comprises causing the obtained dendritic cells to present the  
 PT antigen.  
 XX  
 PS Disclosure; Page 30-32; 32pp; English.  
 XX  
 CC The present invention relates to a method of producing a population of



XX  
 FH Key Location/Qualifiers  
 FT Domain 1. .47  
 FT /note= "putative cytoplasmic domain"  
 FT Domain 48. .68  
 FT /note= "putative transmembrane signal-anchor"  
 FT Domain 69. .317  
 FT /note= "putative extracellular domain"  
 FT Modified-site 171  
 FT /note= "potential N-glycosylation site"  
 FT Modified-site 198  
 FT /note= "potential N-glycosylation site"  
 XX  
 PN WO200276507-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 06-FEB-2002; 2002WO-US001238.  
 XX  
 PR 23-MAR-2001; 2001US-0278215P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Grewal I;  
 XX  
 DR WPI; 2003-058352/05.  
 DR N-PSDB; ABV75842.  
 XX  
 PT Stimulating mammalian monocytes by exposing to an OPG ligand polypeptide,  
 PT useful for treating immune related disorders such as autoimmune disease,  
 PT rheumatoid arthritis, diabetes, osteoarthritis, psoriasis, and allergy.  
 XX  
 PS Claim 1; Fig 1B; 111pp; English.  
 XX  
 CC The present sequence is the protein sequence of human osteoprotegerin  
 CC ligand (OPGL), a member of the tumour necrosis factor (TNF) family of  
 CC molecules that has been reported to bind to at least 2 receptors, RANK  
 CC and OPG. In the present invention, OPGL was shown to activate human  
 CC monocytes, and to activate such monocytes to secrete certain cytokines  
 CC such as interleukin-1 (IL-1), IL-6, IL-12, MIP-1alpha and TNF-alpha and  
 CC chemokines such as IL-8. OPGL may function in up-regulation of co-  
 CC stimulatory molecules such as ICAM-a and VCAM-1, LFA, and B7.1, B7.3 and  
 CC B7h. OPGL may also serve as an antigen presenting molecule which enhances  
 CC T-cell activation. The invention provides methods of using OPGL to  
 CC activate monocytes to secrete chemokines or cytokines by exposing a  
 CC mammalian cell (in cell culture or in a mammal) to OPGL. Also provided  
 CC are methods of using OPGL to treat conditions or diseases in mammals  
 CC associated with, or resulting from lack of, or decreased, chemokine or  
 CC cytokine secretion by monocytes. The invention also provides agonist and  
 CC antagonist molecules to modulate immune activity. These may include  
 CC antibodies to the OPG or RANK receptors. An antagonist comprising an anti-  
 CC -OPGL antibody, an anti-OPG receptor antibody, an anti-RANK receptor  
 CC antibody, an OPG receptor immunoadhesin or a RANK receptor immunoadhesin  
 CC is used in a claimed method of treating an immune-related condition,  
 CC especially an autoimmune disease, rheumatoid arthritis, insulin dependent  
 CC diabetes, osteoarthritis, inflammatory bowel disease (especially  
 CC ulcerative colitis or Crohn's disease), psoriasis, transplant rejection

CC or allergy  
XX  
SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 14

AAE34364

ID AAE34364 standard; protein; 317 AA.

XX

AC      AAE34364;

XX

DT 14-MAY-2003 (first entry)

XX

DE Human receptor activator of NF-kappa B ligand (RANKL).

XX

KW Human; acute septic arthritis; osteomalacia; hyperparathyroidism;  
KW Cushing's syndrome; receptor activator of NF-kappa B ligand; cancer;  
KW bone formation; rickets; Langerhan's cell histiocytosis; gene therapy;  
KW monoostotic fibrous dysplasia; radiation therapy; spinal cord injury;  
KW RANKL; Gaucher's disease; polyostotic fibrous dysplasia; scurvy.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Domain	1. .47
----	--------	--------

```
FT                               /note= "Intracellular domain"
```

FT	Domain	48.	.68
----	--------	-----	-----

```
FT                               /note= "Transmembrane domain"
```

FT Domain 69. .317

FT /note= "Extracellular domain"  
 FT Binding-site 162. .317  
 FT /note= "RANK-binding domain"  
 XX  
 PN WO200292016-A2.  
 XX  
 PD 21-NOV-2002.  
 XX  
 PF 17-MAY-2002; 2002WO-US016002.  
 XX  
 PR 17-MAY-2001; 2001US-0291919P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Dougall WC, Anderson DM;  
 XX  
 DR WPI; 2003-129220/12.  
 DR N-PSDB; AAD52598.  
 XX  
 PT Treating patients having e.g. acute septic arthritis, osteomalacia,  
 PT hyperparathyroidism, Cushing's syndrome or spinal cord injury, comprises  
 PT administering a receptor activator of NF-kappa B antagonist to increase  
 PT bone formation.  
 XX  
 PS Claim 1; Page 51-52; 52pp; English.  
 XX  
 CC The invention relates to a method of treating a patient having e.g. acute  
 CC septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome  
 CC or spinal cord injury. The method involves administering a receptor  
 CC activator of NF-kappa B (RANK) antagonist to stimulate an increase in the  
 CC rate for formation of new bone. RANK antagonist is capable of inhibiting  
 CC the ability of RANK to induce NF-kappa B. The method is useful for  
 CC stimulating bone formation, or for treating patients having acute septic  
 CC arthritis, osteomalacia (including rickets and scurvy),  
 CC hyperparathyroidism, Cushing's syndrome, monoostotic fibrous dysplasia,  
 CC polyostotic fibrous dysplasia, Gaucher's disease, Langerhan's cell  
 CC histiocytosis, spinal cord injury, patients requiring periodontal  
 CC reconstruction, or patients who have completed a course or radiation  
 CC therapy for cancer. The method is also useful for treating a patient who  
 CC is a prosthetic joint recipient, a bone graft recipient, or a ligament  
 CC graft recipient. The invention is useful in gene therapy. The present  
 CC sequence is human RANK ligand (RANKL) protein  
 XX  
 SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120



Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 15

ABR42314

ID ABR42314 standard; protein; 317 AA.  
 XX  
 AC ABR42314;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Human RANKL protein.  
 XX  
 KW Human; RANKL; tumour necrosis factor; ligand; cytostatic;  
 KW immunomodulator; osteopathic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003040307-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 25-JUL-2002; 2002WO-US023782.  
 XX  
 PR 27-JUL-2001; 2001US-0307838P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Hilbert DH, Rosen CA;  
 XX  
 DR WPI; 2003-430659/40.  
 XX  
 PT New heteromultimeric complex having a first polypeptide member of the  
 PT tumor necrosis factor (TNF) ligand family, and a second different member  
 PT of TNF ligand family, useful for treating cancer, osteoporosis or an  
 PT autoimmune disease.  
 XX  
 PS Disclosure; Page 366-367; 388pp; English.  
 XX  
 CC The present sequence is the protein sequence of human RANKL protein. The  
 CC invention relates to compositions comprising heterotrimeric complexes of  
 CC tumour necrosis factor (TNF) ligand family members, and their use in the  
 CC detection, prevention and treatment of disease. In one embodiment, the

CC heterotrimeric complex comprises full-length or extracellular portions of  
 CC RANKL and full-length or extracellular portions of other TNF ligand  
 CC family members, preferably TRAIL. The heterotrimeric complexes of the  
 CC invention are useful for treating an autoimmune disease, cancer or  
 CC osteoporosis, and particularly for inhibiting cancer cell proliferation,  
 CC increasing B cell proliferation, or inducing apoptosis of T cells. A  
 CC claimed method of inhibiting cancer cell proliferation comprises  
 CC administering a heterotrimeric complex consisting of TRAIL and CD40L or  
 CC RANKL. A claimed method of treating osteoporosis comprises administering  
 CC an antibody against a complex comprising RANKL and TRAIL

XX

SQ Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 6; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-154;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV	60
Qy	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Db	121	QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

Search completed: February 25, 2004, 16:28:58  
 Job time : 65 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2004, 16:27:52 ; Search time 23 Seconds  
(without alignments)  
711.541 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1685	100.0	317	3	US-08-996-139-13	Sequence 13, Appl
2	1685	100.0	317	3	US-08-995-659-13	Sequence 13, Appl
3	1685	100.0	317	3	US-09-215-649A-13	Sequence 13, Appl
4	1685	100.0	317	4	US-09-052-521C-4	Sequence 4, Appli
5	1685	100.0	317	4	US-09-577-780-13	Sequence 13, Appl
6	1685	100.0	317	4	US-09-577-800-13	Sequence 13, Appl
7	1685	100.0	317	4	US-09-466-496-13	Sequence 13, Appl
8	1685	100.0	317	4	US-09-871-856-13	Sequence 13, Appl
9	1685	100.0	317	4	US-09-871-291-13	Sequence 13, Appl
10	1685	100.0	317	4	US-09-396-937-2	Sequence 2, Appli
11	1685	100.0	317	4	US-09-877-650-13	Sequence 13, Appl

12	1417.5	84.1	316	2	US-08-842-842-7	Sequence 7, Appli
13	1417.5	84.1	316	3	US-08-989-362-2	Sequence 2, Appli
14	1417.5	84.1	316	4	US-09-052-521C-2	Sequence 2, Appli
15	1417.5	84.1	316	4	US-09-671-658A-2	Sequence 2, Appli
16	1417.5	84.1	316	4	US-09-396-937-4	Sequence 4, Appli
17	1417.5	84.1	316	4	US-09-396-937-6	Sequence 6, Appli
18	1326.5	78.7	294	3	US-08-996-139-11	Sequence 11, Appl
19	1326.5	78.7	294	3	US-08-995-659-11	Sequence 11, Appl
20	1326.5	78.7	294	3	US-09-215-649A-11	Sequence 11, Appl
21	1326.5	78.7	294	4	US-09-577-780-11	Sequence 11, Appl
22	1326.5	78.7	294	4	US-09-577-800-11	Sequence 11, Appl
23	1326.5	78.7	294	4	US-09-466-496-11	Sequence 11, Appl
24	1326.5	78.7	294	4	US-09-871-856-11	Sequence 11, Appl
25	1326.5	78.7	294	4	US-09-871-291-11	Sequence 11, Appl
26	1326.5	78.7	294	4	US-09-877-650-11	Sequence 11, Appl
27	771	45.8	187	4	US-09-396-937-8	Sequence 8, Appli
28	769	45.6	173	4	US-09-396-937-10	Sequence 10, Appl
29	759	45.0	173	4	US-09-396-937-12	Sequence 12, Appl
30	721.5	42.8	188	4	US-09-396-937-14	Sequence 14, Appl
31	711.5	42.2	182	4	US-09-396-937-16	Sequence 16, Appl
32	691	41.0	173	4	US-09-396-937-18	Sequence 18, Appl
33	670	39.8	173	4	US-09-396-937-20	Sequence 20, Appl
34	418	24.8	77	4	US-09-632-287A-11	Sequence 11, Appl
35	363	21.5	77	4	US-09-632-287A-10	Sequence 10, Appl
36	251.5	14.9	279	4	US-09-072-993C-3	Sequence 3, Appli
37	251.5	14.9	281	1	US-08-670-354-2	Sequence 2, Appli
38	251.5	14.9	281	3	US-08-584-031-1	Sequence 1, Appli
39	251.5	14.9	281	3	US-08-780-496-1	Sequence 1, Appli
40	251.5	14.9	281	3	US-08-883-086-10	Sequence 10, Appl
41	251.5	14.9	281	3	US-09-320-424-2	Sequence 2, Appli
42	251.5	14.9	281	4	US-09-333-593A-6	Sequence 6, Appli
43	251.5	14.9	281	4	US-09-157-864-11	Sequence 11, Appl
44	251.5	14.9	281	4	US-09-825-563-2	Sequence 2, Appli
45	251.5	14.9	281	4	US-10-039-785-66	Sequence 66, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-996-139-13

; Sequence 13, Application US/08996139

; Patent No. 6017729

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

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Query Match          100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
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Qy    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
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Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300
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Qy    301 PDQDATYFGAFKVRDID 317

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Db

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301 PDQDATYFGAFKVRDID 317

RESULT 2

US-08-995-659-13

; Sequence 13, Application US/08995659

; Patent No. 6242213

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/995,659

; FILING DATE: 22 DECEMBER 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-995-659-13

Query Match 100.0%; Score 1685; DB 3; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.6e-163;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
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Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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RESULT 3

US-09-215-649A-13

; Sequence 13, Application US/09215649A

; Patent No. 6271349

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/215,649A

; FILING DATE: 17-Dec-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

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;          FILING DATE: <Unknown>
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;  ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2851-A
;  TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;  INFORMATION FOR SEQ ID NO: 13:
;  SEQUENCE CHARACTERISTICS:
;          LENGTH: 317 amino acids
;          TYPE: amino acid
;          TOPOLOGY: linear
;  MOLECULE TYPE: protein
;  SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

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Query Match          100.0%;  Score 1685;  DB 3;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 2.6e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQD TTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
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Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240
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Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317

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RESULT 4

US-09-052-521C-4

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; Sequence 4, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors

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; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4
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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
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Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQIMV 240
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Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
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Db    301 PDQDATYFGAFKVRDID 317
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# RESULT 5

US-09-577-780-13

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; Sequence 13, Application US/09577780
; Patent No. 6419929
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## GENERAL INFORMATION:

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; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
```

```

;          CITY: Seattle
;          STATE: WA
;          COUNTRY: USA
;          ZIP: 98101
;
;  COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: Apple Power Macintosh
;          OPERATING SYSTEM: Apple Operating System 7.5.5
;          SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
;  CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/577,780
;          FILING DATE: 24-May-2000
;          CLASSIFICATION: <Unknown>
;
;  PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/995,659
;          FILING DATE: <Unknown>
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
;
;  ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2852-A
;
;  TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
;
;  INFORMATION FOR SEQ ID NO: 13:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 317 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13

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```

Query Match          100.0%;  Score 1685;  DB 4;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 2.6e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFfKLRSGEESIEVSNPSLLD 300

```

```

Db          241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
Qy          301 PDQDATYFGAFKVRDID 317
           |||||
Db          301 PDQDATYFGAFKVRDID 317

```

RESULT 6

US-09-577-800-13

; Sequence 13, Application US/09577800

; Patent No. 6479635

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; APPLICANT: Galibert, Laurent

; APPLICANT: Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/577,800

; FILING DATE: 24-MAY-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/996,139

; FILING DATE: 22 DECEMBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-577-800-13

Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.6e-163;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
          |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
          |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
          |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQIMV 240
          |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQIMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
          |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
          |||
Db    301 PDQDATYFGAFKVRDID 317
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RESULT 7

US-09-466-496-13

; Sequence 13, Application US/09466496

; Patent No. 6528482

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/466,496

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;          FILING DATE: 17-Dec-1999
;          CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/996,139
;          FILING DATE: 22 DECEMBER 1997
;          APPLICATION NUMBER: USSN 60/064,671
;          FILING DATE: 14 OCTOBER 1997
;          APPLICATION NUMBER: USSN 08/813,509
;          FILING DATE: 07 MARCH 1997
;          APPLICATION NUMBER: USSN 08/772,330
;          FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
;          NAME: Perkins, Patricia Anne
;          REGISTRATION NUMBER: 34,693
;          REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206)587-0430
;          TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 317 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-466-496-13

```

```

Query Match          100.0%;  Score 1685;  DB 4;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 2.6e-163;
Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 8



Db	61	VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK	120
Qy	121	QAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Db	121	QAFQGA VQKELQHIVGSQHIRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGSH	180
Qy	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV	240
Db	181	KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV	240
Qy	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Db	241	YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD	300
Qy	301	PDQDATYFGAFKVRDID	317
Db	301	PDQDATYFGAFKVRDID	317

RESULT 9

US-09-871-291-13

; Sequence 13, Application US/09871291

; Patent No. 6562948

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/871,291

; FILING DATE: 30-May-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/996,139

; FILING DATE: <Unknown>

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2851-A

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-291-13
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Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        |||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        |||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180
        |||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240
        |||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        |||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        |||
Db    301 PDQDATYFGAFKVRDID 317
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RESULT 10

US-09-396-937-2

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; Sequence 2, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-396-937-2
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Query Match 100.0%; Score 1685; DB 4; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.6e-163;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPAAASRSMFVALLGLGLGQV 60 
Db	1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPAAASRSMFVALLGLGLGQV 60
Qy	61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQD TKLIPDSCRRIK 120 
Db	61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQD TKLIPDSCRRIK 120
Qy	121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHL TINAT DIPSGSH 180 
Db	121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHL TINAT DIPSGSH 180
Qy	181 KVSLSWYHDRGWAKISNM TFSNGKLIVNQDG FYYLYANICFRHHETS GD LATE YLQLMV 240 
Db	181 KVSLSWYHDRGWAKISNM TFSNGKLIVNQDG FYYLYANICFRHHETS GD LATE YLQLMV 240
Qy	241 YVTKT SIK IPSSHTLMKG GSTKYWSGNSEFH FY SINVG GFFKLR SGEE ISIEVS NP SL LD 300 
Db	241 YVTKT SIK IPSSHTLMKG GSTKYWSGNSEFH FY SINVG GFFKLR SGEE ISIEVS NP SL LD 300
Qy	301 PDQDATYFGA FKVR DID 317 
Db	301 PDQDATYFGA FKVR DID 317

RESULT 11

US-09-877-650-13

; Sequence 13, Application US/09877650

; Patent No. 6649164

; GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

Maraskovsky, Eugene

7 TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

```

;      NUMBER OF SEQUENCES: 19

```

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

; CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

```

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;          COMPUTER: Apple Power Macintosh
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; OPERATING SYSTEM: Apple Operating System 7.5.5
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SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

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; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/877,650
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: 1997-12-22
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

```

```

Query Match          100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 2.6e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180

Qy    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYQLQMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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RESULT 12  
 US-08-842-842-7

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; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
;   APPLICANT: Boyle, William J.
;   TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Amgen Inc.
;     STREET: 1840 Dehavilland Drive
;     CITY: Thousand Oaks
;     STATE: California
;     COUNTRY: USA
;     ZIP: 91230-1789
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/842,842
;     FILING DATE:
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Winter, Robert B.
;     REFERENCE/DOCKET NUMBER: A-451
;   INFORMATION FOR SEQ ID NO: 7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 316 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-842-842-7

```

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Query Match          84.1%; Score 1417.5; DB 2; Length 316;
Best Local Similarity 84.3%; Pred. No. 4.6e-136;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

```

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59
        ||||| ||| ||||| ||| ||||| || ||| ||||| |||||:|||||
Db      1 MRRASRDYGKYLRSSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy      60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
        |||:||| ||||| ||||| ||| ||||| || ||:||||:| :||||:
Db      61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCR RM 118

Qy      120 KQAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179
        ||||| ||||| ||| |||:||||:|:| ||||| |||||
Db      119 KQAFQGA VQKELQHIVGPPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHTINAASIPSGS 178

Qy      180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
        |||:||||| ||||| ||||| ||||| ||||| |||||:|:||||
Db      179 HKVTLSSWYHDRGWAKISNMTLSNGKLVRNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy      240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFKLRSGEEISIEVSNPSSL 299
        ||| ||||| ||||| ||||| ||||| |||||:||||:||||
Db      239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFKLRAGEEISIQVSNPSSL 298

```

Qy 300 DPDQDATYFGAFKVRDID 317  
|||||||:||||  
Db 299 DPDQDATYFGAFKVQDID 316

RESULT 13

US-08-989-362-2

; Sequence 2, Application US/08989362

; Patent No. 6242586

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; APPLICANT: Mattson, Jeanine D.

; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related

; TITLE OF INVENTION: Reagents

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/989,362

; FILING DATE: 12-DEC-1997

; CLASSIFICATION: 56

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/032,846

; FILING DATE: 13-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0686

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650)852-9196

; TELEFAX: (650)496-1204

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 316 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-989-362-2

Query Match 84.1%; Score 1417.5; DB 3; Length 316;

Best Local Similarity 84.3%; Pred. No. 4.6e-136;

Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59  
||||||| |||| |||| ||| |||||| || ||| |||||||:|||||||  
Db 1 MRRASRDYGYKLYRSSEEMGGSGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLI	PDSCRR	119																																								
Db	61	VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM		118																																								
Qy	120	KQAFQGA	VQKELQHIVGSQH	IRA	EKAMVDG	SWLDLAKR	SKLEA	QPF	AHLT	INAT	DIPSGS	179																																
Db	119	KQAFQGA	VQKELQHIVGPQ	R	FSGAPAMMEG	SWLDVAQ	R	GKPEA	QPF	AHLT	INAAS	DIPSGS	178																															
Qy	180	HKVSLSSWYH	D	R	G	WAKIS	NMTFS	N	G	K	L	I	V	N	Q	D	G	F	Y	Y	L	A	N	I	C	F	R	H	H	E	T	S	G	D	L	A	T	E	Y	L	Q	L	M	239
Db	179	HKVTLSSWYH	D	R	G	WAKIS	NMTLS	N	G	K	L	R	V	N	Q	D	G	F	Y	Y	L	A	N	I	C	F	R	H	H	E	T	S	G	S	V	P	T	D	Y	L	Q	L	M	238
Qy	240	VYVTKTSI	KIPSS	HTLMKGG	STKYW	SGNSE	FHFYS	I	N	V	G	G	F	F	K	L	R	S	G	E	E	I	S	I	E	V	S	N	P	S	L	L	299											
Db	239	VYVVKTSI	KIPSS	HNLMKGG	STKNW	SGNSE	FHFYS	I	N	V	G	G	F	F	K	L	R	A	G	E	E	I	S	I	Q	V	S	N	P	S	L	L	298											
Qy	300	DPDQDATY	F	G	A	F	K	V	R	D	I	D	317																															
Db	299	DPDQDATY	F	G	A	F	K	V	Q	D	I	D	316																															

Db 119 KQAFQGA VQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPF AHLTINAASIPSGS 178

Qy 180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239  
 |||:||||| ||||| ||||| ||||| ||||| ||||| : |:|||||

Db 179 HKVTLSSWYHDRGWAKISNMTLSNGKL RVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLL 299  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| : |||||

Db 239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVG GFFKLRAGEEISIQVSNPSLL 298

Qy 300 DPDQDATYFGAFKVRDID 317  
 ||||| ||||| : |||

Db 299 DPDQDATYFGAFKVQDID 316

RESULT 15

US-09-671-658A-2

; Sequence 2, Application US/09671658A

; Patent No. 6525180

; GENERAL INFORMATION:

; APPLICANT: Gorman, Daniel M.

; Mattson, Jeanine D.

; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related  
 ; Reagents

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DNAX Research Institute

; STREET: 901 California Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/671,658A

; FILING DATE: 27-Sep-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/989,362

; FILING DATE: 12-DEC-1997

; APPLICATION NUMBER: US 60/032,846

; FILING DATE: 13-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ching, Edwin P.

; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0686

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650)852-9196

; TELEFAX: (650)496-1204

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 316 amino acids

; TYPE: amino acid

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;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-671-658A-2
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Query Match          84.1%;  Score 1417.5;  DB 4;  Length 316;
Best Local Similarity 84.3%;  Pred. No. 4.6e-136;
Matches 268;  Conservative 16;  Mismatches 31;  Indels 3;  Gaps 2;
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```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59
          ||||| ||| |||| ||| ||||| || ||| |||||:|||||
Db      1 MRRASRDYGKYLRSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy     60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
          |||:| ||||| ||||| ||| ||||| ||:| |||:| :|||:
Db     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRRM 118

Qy    120 KQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPFAHLTINATDIPSGS 179
          ||||| ||||| ||| ||:| ||||:|:| ||||| |||||
Db    119 KQAFQGA VQKELQHIVGPGRFSGAPAMMEG SWLDVAQRGKPEAQPFALTINAASIPSGS 178

Qy    180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
          |||:| ||||| ||||| ||||| ||||| ||||| ||||| :|:| |||
Db    179 HKVTLSSWYHDRGWAKISNMTLSNGKL RVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy    240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299
          ||| ||||| ||||| ||||| ||||| ||||| ||||| :|||:| |||||
Db    239 VYVVKTSIKIPSSHNLKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298

Qy    300 DPDQDATYFGAFKVRDID 317
          ||||| ||||| |||
Db    299 DPDQDATYFGAFKVQDID 316
```

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Search completed: February 25, 2004, 16:31:35
Job time : 25 secs
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OM protein - protein search, using sw model

Run on: February 25, 2004, 16:25:52 ; Search time 20 Seconds  
(without alignments)  
1524.636 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	189	11.2	281	2	I38707	Fas ligand - human
2	184.5	10.9	279	2	A53062	Fas ligand - mouse
3	176.5	10.5	261	2	S53090	CD40 ligand - bovi
4	175.5	10.4	278	2	A49266	fas ligand - rat
5	158.5	9.4	261	2	I53476	CD40 ligand - huma
6	141.5	8.4	235	1	QWMSN	tumor necrosis fac
7	141	8.4	234	1	A25451	tumor necrosis fac
8	137	8.1	234	1	JH0529	tumor necrosis fac
9	133	7.9	233	1	QWHUN	tumor necrosis fac
10	132.5	7.9	235	2	I54490	tumor necrosis fac
11	131.5	7.8	235	2	JU0029	tumor necrosis fac
12	130.5	7.7	306	2	I49139	lymphotoxin-beta -
13	130	7.7	233	1	S22052	tumor necrosis fac



14	128	7.6	234	1	JQ1344	tumor necrosis fac
15	126.5	7.5	233	1	S24642	tumor necrosis fac
16	126	7.5	232	1	S12606	tumor necrosis fac
17	125.5	7.4	185	2	S52715	tumor necrosis fac
18	122	7.2	193	2	S06192	tumor necrosis fac
19	120	7.1	260	2	S21738	CD40 ligand - mous
20	117	6.9	233	2	S11688	tumor necrosis fac
21	117	6.9	244	2	A46066	lymphotoxin beta -
22	97.5	5.8	1464	1	CGHU1S	collagen alpha 1(I
23	94.5	5.6	664	2	C84747	probable protein k
24	92.5	5.5	205	1	QWHUX	lymphotoxin alpha
25	92.5	5.5	450	2	S38114	hypothetical prote
26	91.5	5.4	3848	2	T17414	TipC protein - sli
27	91	5.4	493	2	AC0937	probable GntR-fami
28	90.5	5.4	1694	2	S50065	sialoadhesin - mou
29	90	5.3	730	2	JC1456	gelatinase B (EC 3
30	89.5	5.3	331	2	AF3526	homoprotocatechuat
31	89.5	5.3	379	2	A47659	farnesyl-protein t
32	89	5.3	202	1	B27303	tumor necrosis fac
33	89	5.3	440	2	I49681	glyceraldehyde-3-p
34	89	5.3	479	2	A25052	fibrinogen beta ch
35	89	5.3	639	2	C83624	probable two-compo
36	88.5	5.3	565	2	C89893	hypothetical prote
37	88.5	5.3	578	2	S51379	probable phosphoes
38	88.5	5.3	684	2	T01267	leucine-rich repea
39	88.5	5.3	883	2	A49733	[heparan sulfate]-
40	87.5	5.2	610	2	T06690	galactonolactone d
41	87.5	5.2	1466	1	CGHU7L	collagen alpha 1(I
42	87	5.2	639	2	A32935	protein P1 - Entam
43	87	5.2	1114	2	JH0284	125K surface antig
44	87	5.2	1315	2	G96722	hypothetical prote
45	86.5	5.1	279	2	F72339	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

I38707

Fas ligand - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000

C;Accession: I38707; JC2340; S57565; I38554

R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A;Title: Human Fas ligand: gene structure, chromosomal location and species specificity.

A;Reference number: I38707; MUID:95127560; PMID:7826947

A;Accession: I38707

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-281 <RES>

A;Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431

R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioaka, T.; Kasahara, A.;

Fusamoto, H.; Kamada, T.

Biochem. Biophys. Res. Commun. 204, 468-474, 1994

A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.

A;Reference number: JC2340; MUID:95071350; PMID:7980502  
 A;Accession: JC2340  
 A;Molecule type: DNA  
 A;Residues: 1-281 <MIT>  
 A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1;  
 PID:g1369902  
 R;Schatzlein, C.E.  
 submitted to the EMBL Data Library, June 1995  
 A;Reference number: S57565  
 A;Accession: S57565  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-281 <SCH>  
 A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456  
 R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley,  
 K.A.; Goodwin, R.G.; Smith, C.A.; Ramsdell, F.; Lynch, D.H.  
 J. Exp. Med. 181, 71-77, 1995  
 A;Title: Fas ligand mediates activation-induced cell death in human T  
 lymphocytes.  
 A;Reference number: I38554; MUID:95105731; PMID:7528780  
 A;Accession: I38554  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-281 <RE2>  
 A;Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628  
 C;Genetics:  
 A;Gene: FasL  
 A;Introns: 151/1; 116/3  
 C;Keywords: glycoprotein; transmembrane protein  
 F;80-102/Domain: transmembrane #status predicted <TMM>  
 F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.2%; Score 189; DB 2; Length 281;  
 Best Local Similarity 21.7%; Pred. No. 1.9e-08;  
 Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

Qy	22	PGAPHEGPLHAPPPAP----	HQPPAASRS-----	MFVALLGLGLGQVVCS	63
				:	
Db	46	PPPPPPPLPPPPPPPLPPLPLPPLKRGNHSTGLCLLMFFMVLVALVGLGLG-----			100
Qy	64	VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRKQAF			123
		:	: : :   :		
Db	101	--MFQLFHLQ-----	KELAELESTSQMHTA-----		124
Qy	124	QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSHK			181
		: : :   :	:         : :		
Db	125	--SSLEKQIGH-----	PSPPPEKKELRKVAHLTGKSNRSRMP-----		159
Qy	182	VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMVY			241
		: : :     : : :     :			
Db	160	---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----		LPLSHK	210
Qy	242	VTKTSIKIPSSHTLMKGGSTKY-----	WSGNSEFHFYSINVGGFFKLRSGEIEISIEVSN		295
		:     :       :	:       : :		
Db	211	VYMRNSKYPQDLVMEGKMMSYCTTGQMWARSS-----	YLGAVENLTSADHLYVNVSE		263
Qy	296	PSLLDPDQDATYFGAFKV			313

||:: :: |::| ::  
Db 264 LSLVNFEEESQTFFGLYKL 281

RESULT 2

A53062

Fas ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

C;Accession: A53062

R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagata, S.

Cell 76, 969-976, 1994

A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.

A;Reference number: A53062; MUID:94185175; PMID:7511063

A;Accession: A53062

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-279 <TAK>

A;Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 10.9%; Score 184.5; DB 2; Length 279;  
Best Local Similarity 21.7%; Pred. No. 4.6e-08;  
Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

Qy 13 RGSEEMGGPGAPHEGPLHAPPPAPHP-----PAASRSMFVALLGLGL 57  
|| :: | | | | | | | | : ||::||  
Db 38 RGPDQRRPPPPPPVSPPLPPSQPLPLPLTPLKKKDHNNTNLWLPVVFFMVLVALVGMGL 97  
  
Qy 58 GQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117  
| :||: |  
Db 98 G-----MYQLFHL----- 105  
  
Qy 118 RIKQAFQGA VQKELQHI--VGSQHRA---EKAMVDGSWLDLAKRSKLEAQPFAHLTINA 172  
|||| : :| :: || : : | | : |||| |  
Db 106 -----QKELAELEFTNQSLKVSSFQKQIANPS----TPSEKKEPRSVAHLTGN-- 150  
  
Qy 173 TDIPSGSHKVSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231  
| | : | | || : : | |::| : || :  
Db 151 -----PHSRSIPLWEDTYGTALISGVKYKGGGLVINETGLYFVYSKVYFRGQSCN--- 201  
  
Qy 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEHFYSINVGGFFKLRSGE EISI 291  
: | ||: : | | ||: | : : :| :| ||| : : :  
Db 202 -NQPLNHKVYMRNS--KYPEDLVLMEERLNYCT-TGQIWAHSSYLGA VFNLT SADHLYV 257  
  
Qy 292 EVSNPSLLDPDQDATYFGAFKV 313  
:| ||:: :: |::| ::  
Db 258 NISQLSLINFEEESKTFFGLYKL 279

RESULT 3

S53090

CD40 ligand - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 05-Nov-1999

C;Accession: S53090

R;Mertens, B.E.L.C.; Muriuki, M.  
submitted to the EMBL Data Library, February 1995  
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.  
A;Reference number: S53090  
A;Accession: S53090  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <MER>  
A;Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g732570

Query Match 10.5%; Score 176.5; DB 2; Length 261;  
Best Local Similarity 24.2%; Pred. No. 2e-07;  
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

```

Qy      33 PPPPAPHQPPAASRSMFVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL 91
      | | :   | | :| : | | :|   |   |   :| :| :| :|
Db      8 PSPRS VATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----R 57

Qy      92 RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG 149
      |||: | |   : |   :| | : | : | :|   : : : : :| :
Db      58 NLHEDFVFMKTIQRCNKGEGLSLLNCEEIRSRFEDLVKDIMQ----NKEVKKKEKNFE- 112

Qy     150 SWLDLAKRSKLEAQPF AHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-L 206
      :   | | || : | :   | | : | :| :| :| | || |
Db     113 -----MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYITLSNNLVTLENGKQL 161

Qy     207 IVNQDGFYIYLANICFRHHETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKYW 264
      | : |||| :| : | :   | |   : :   :| | | | : : :|
Db     162 AVKRQGFYIYTQVTFCSNR-----ETLSQAPFIASLCLKSPSGSERILLRAANTH-- 212

Qy     265 SGNSEFHFYSINVGFFKLRSGEIEISIEVSNPSLLDPDQDATYFGAFKV 313
      | :   || :|| | :| :| : : | :|| :   | || | :
Db     213 SSSKPCGQQSIHLGGVFELQSGASVFNVTDP SQVSHGTGFTSFGLLKL 261

```

#### RESULT 4

A49266

fas ligand - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

C;Accession: A49266

R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.

Cell 75, 1169-1178, 1993

A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.

A;Reference number: A49266; MUID:94084792; PMID:7505205

A;Accession: A49266

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-278 <SUD>

A;Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179

C;Keywords: glycoprotein; transmembrane protein

Query Match 10.4%; Score 175.5; DB 2; Length 278;  
Best Local Similarity 20.3%; Pred. No. 2.7e-07;  
Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

Qy	21	GPGAPHEGPLHAPPPAPHQPPAASRSM-----FVALLGLGL	57
		:   : :   :   :   :   :   :   :	
Db	39	GPGQRRPPP--PPPPSPLPPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGL	96
Qy	58	GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR	117
		: :     : :     :   : :     : : : :	
Db	97	G-----MYQLFHLLQKELAELEFREFTNHSL-RVSSFEKQIANPSTPSETKKPRSV-----	143
Qy	118	RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLIDLAKRSKLEAQPFALHTINATDI PS	177
Db	144	-----AHLTG NPR----	151
Qy	178	GSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFIYYLYANICFRHHETSGDLATEYLQ	237
		:         : :   : : :   : : : :   : : :	
Db	152	-SRSIPL-EWEDTYGTALISGVKYKKGGGLVINEAGLYFVYSKVYFRGQSCN----SQPLS	205
Qy	238	LMVYVTKTTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVS NPS	297
		: :       : :   : : :     : : : :	
Db	206	HKVYM--RNFKYPGDLVLMEEKKKNYCT-TGQIWAHSSYLGA VFNLT VADHLYVNISQLS	262
Qy	298	LLDPDQDATYFGAFKV	313
		: : :   :   :   :	
Db	263	LINFEEKSTFFGLYKL	278

A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.  
 A;Reference number: S26694; MUID:93076854; PMID:1280226  
 A;Accession: S26694  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-261 <GRA>  
 A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270  
 R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.Y.  
 FEBS Lett. 315, 259-266, 1993  
 A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of expression by factors controlling IgE production.  
 A;Reference number: S28852; MUID:93138085; PMID:7678552  
 A;Accession: S28852  
 A;Molecule type: mRNA  
 A;Residues: 1-261 <GAU>  
 A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124  
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln  
 C;Genetics:  
 A;Gene: GDB:CD40LG; HIGM1; IMD3  
 A;Cross-references: GDB:120632; OMIM:308230  
 A;Map position: Xq26-Xq26  
 C;Keywords: glycoprotein; transmembrane protein  
 F;13-44/Domain: transmembrane #status predicted <TMM>  
 F;45-261/Domain: extracellular #status predicted <EXT>  
 F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 158.5; DB 2; Length 261;  
 Best Local Similarity 24.5%; Pred. No. 6.8e-06;  
 Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

```

Qy      45 SRSMFVALLGLGL-GQVVC SVALFFYFRAQMDPNRI SEDGTHCIYRILRLHENADFQDT- 102
      | :|: || : | |:: |      | :| :| ::      |||: | |
Db      20 SMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----RNLHEDFVFMKTI 69

Qy     103 -TLESQDTKLIPDSCRRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLE 161
      : : | :| || |:: | |:: : | :| :| :: | :
Db      70 QRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEETKKENSF-EMQKGDQ-N 119

Qy     162 AQPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYYLYA 218
      | ||: |: | | :| :|: || :| ||| | | : | ||: ||
Db     120 PQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYA 173

Qy     219 NICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWSGNSEFHFYSIN 276
      : | : : |      :: :| |      |:: :| |      ||:
Db     174 QVTFC SNREASSQAP-----FIASLCLKSPGRFERILLRAANTH--SSAKPCGQQSIH 224

Qy     277 VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
      :|| |::| | : : |::|| :      | || |:
Db     225 LGGVFELQPGASVFNVTDP SQVSHGTGFTSFGLLKL 261
  
```

# RESULT 6

QWMSN

tumor necrosis factor alpha precursor - mouse

N;Alternate names: cachectin; TNF alpha

C;Species: Mus musculus (house mouse)  
 C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 04-Feb-2000  
 C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696  
 R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.  
 DNA 7, 193-201, 1988  
 A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor.  
 A;Reference number: A22908; MUID:88224564; PMID:2836146  
 A;Accession: A22908  
 A;Molecule type: DNA  
 A;Residues: 1-235 <SHI>  
 A;Cross-references: GB:M20155  
 R;Shakhov, A.N.; Nedospasov, S.A.  
 Bioorg. Khim. 13, 701-705, 1987  
 A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucleotide sequence of the genomic copy of TNF-alpha in mice.  
 A;Reference number: S03791; MUID:87298639; PMID:3040015  
 A;Accession: S03791  
 A;Molecule type: DNA  
 A;Residues: 1-235 <SHA>  
 A;Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087  
 A;Note: article in Russian with English abstract  
 R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.  
 Nucleic Acids Res. 15, 9083-9084, 1987  
 A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha- (tumor necrosis factor) and TNF-beta-(lymphotoxin) genes.  
 A;Reference number: A93679; MUID:88067722; PMID:3684584  
 A;Accession: A27303  
 A;Molecule type: DNA  
 A;Residues: 1-235 <SEM>  
 A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832  
 R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985  
 A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor.  
 A;Reference number: A25164; MUID:85298296; PMID:3898078  
 A;Accession: A25164  
 A;Molecule type: mRNA  
 A;Residues: 1-235 <PEN>  
 A;Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085  
 R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, E.; Chollet, A.; Tizard, R.; van Heuverswyn, H.; van Vliet, A.; Ruysschaert, M.R.; Fiers, W.  
 Nucleic Acids Res. 13, 4417-4429, 1985  
 A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression.  
 A;Reference number: A23127; MUID:85242112; PMID:2989794  
 A;Accession: A23127  
 A;Molecule type: mRNA  
 A;Residues: 1-235 <FRA>  
 A;Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845  
 R;Cseh, K.; Beutler, B.  
 J. Biol. Chem. 264, 16256-16260, 1989  
 A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in a larger, inactive form of secreted protein.  
 A;Reference number: A34251; MUID:89380231; PMID:2777790  
 A;Accession: A34251

A;Molecule type: protein  
A;Residues: 70-87 <CSE>  
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated  
region of mRNA molecules specifying inflammatory mediators.  
A;Reference number: I59058; MUID:86149365; PMID:2419912  
A;Accession: I59058  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-230,'R',232-235 <RES>  
A;Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083  
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A;Title: Characterization of high molecular weight glycosylated forms of murine  
tumor necrosis factor.  
A;Reference number: A36696; MUID:91097531; PMID:2268312  
A;Accession: A36696  
A;Molecule type: protein  
A;Residues: 80-85,'X',87-99 <SHE>  
C;Genetics:  
A;Introns: 62/3; 81/1; 97/1  
A;Note: the first intron occurs in the 5'-untranslated region  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine;  
macrophage; membrane protein; myristylation  
F;80-235/Product: tumor necrosis factor #status experimental <MAT>  
F;20/Binding site: myristate (Lys) (covalent) #status predicted  
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;148-179/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141.5; DB 1; Length 235;  
Best Local Similarity 25.9%; Pred. No. 0.00017;  
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;

```

Qy      163 QPFAHLTINATDIPSGSHKVLSL-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
      :| ||: |      |:| | | |::| | :::| || |:::
Db      90 KPSVAHVAN-----HQVEEQLEWLSQRANALLANGMDLKDNLVVPADGLYLVYSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
      |:      |      :::| |:::      :::| |      :| | |
Db      142 LFK-----GQGCPDYVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPW----- 192

Qy      269 EFHFYSINVGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
      : |::| |:| |:::| ||: | | : | |
Db      193 ---YEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFG 231

```

# RESULT 7

A25451

tumor necrosis factor alpha precursor - rabbit

N;Alternate names: cachectin; TNF alpha

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C;Accession: A25454; A25451; JS0727



R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.; Kato, M.; Seko, M.  
DNA 5, 149-156, 1986  
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor.  
A;Reference number: A25454; MUID:86219711; PMID:3519137  
A;Accession: A25454  
A;Molecule type: mRNA  
A;Residues: 1-234 <ITO>  
A;Cross-references: GB:M12845; NID:gl65759; PIDN:AAA31486.1; PID:gl65760  
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.  
DNA 5, 157-165, 1986  
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
A;Reference number: A25451; MUID:86219712; PMID:3519138  
A;Accession: A25451  
A;Molecule type: DNA  
A;Residues: 1-234 <IT2>  
A;Note: this sequence differs from that shown in having a Gln inserted between residues 62 and 63  
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
Gene 95, 215-221, 1990  
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis factor).  
A;Reference number: JH0309; MUID:91065534; PMID:2249779  
A;Accession: JS0727  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-62,'Q',63-234 <SHA>  
A;Cross-references: GB:M60340; GB:M35326; NID:gl65754; PIDN:AAA31484.1; PID:gl65756  
C;Genetics:  
A;Introns: 62/3; 80/1; 96/1  
C;Superfamily: tumor necrosis factor  
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
F;1-81/Domain: propeptide #status predicted <PRO>  
F;82-234/Product: tumor necrosis factor #status predicted <MAT>  
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;147-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;  
Best Local Similarity 21.6%; Pred. No. 0.00018;  
Matches 65; Conservative 35; Mismatches 99; Indels 102; Gaps 13;

```

Qy      27 EGPLHAPPPAPHQPPAASR----SMFVALLGLGLGQVVCSSVALFFYFRAQMDPNRISED 82
      |||| | : | |:| || | : | :|| | :
Db      14 EGPL----PKKAGGPQGSKRCLCLSLFSFLLVAGATTLC----LLHFRVIGPQEEESPN 65

Qy      83 GTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRA 142
      | : | | || |
Db      66 NLHLV-----NPVAQMVTLS-----A 82

Qy     143 EKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSHKVSLSWYHGRGWAKISN-MTF 201
      :|: | :| |:| | : : | | :| |
Db      83 SRALSD-----KPLAHVVAN----PQVEGQL---QWLSQRANALLANGMKL 121

```

Qy 202 SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG--- 258  
 ::::| | | : : | | | : : | : : | :  
 Db 122 TDNQLVVPADGLYLIYSQVLF-----SGQGCRSYVLLTHTVSRFAVSYPNKNLLSAIKS 176  
 Qy 259 -----GSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLLD-PDQDATYF 308  
 | : | : | : | : | : | : | : | : | : | :  
 Db 177 PCHRETPEEAEPMAW-----YEPIYLGGVFQLEKGDRLSTEVNQPEYLDLAESGQVYF 229  
 Qy 309 G 309  
 |  
 Db 230 G 230

# RESULT 8

JH0529

tumor necrosis factor alpha precursor - sheep

N;Alternate names: cachectin; TNF alpha

C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C;Accession: JH0529; S48118; S13114; S20661

R;Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with cloning by inverse PCR.

A;Reference number: JH0529; MUID:92112044; PMID:1765267

A;Accession: JH0529

A;Molecule type: mRNA

A;Residues: 1-234 <GRE>

A;Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A;Experimental source: alveolar macrophage

R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A;Reference number: S48118; MUID:92155784; PMID:1786996

A;Accession: S48118

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-234 <NAS>

A;Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A;Reference number: S13114; MUID:91067496; PMID:2251151

A;Accession: S13114

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-62,64-234 <YOU>

A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A;Note: comparison with the introns of homologous sequences suggest that this is probably an alternative splicing

C;Superfamily: tumor necrosis factor

C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myristylation; transmembrane protein

F;1-77/Domain: propeptide #status predicted <PRO>

F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F;20/Binding site: myristate (Lys) (covalent) #status predicted

F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;146-178/Disulfide bonds: #status predicted

Query Match 8.1%; Score 137; DB 1; Length 234;  
Best Local Similarity 26.1%; Pred. No. 0.0004;  
Matches 52; Conservative 30; Mismatches 71; Indels 46; Gaps 10;

Qy 134 IVGSQHRAEKAMVDGSW---LDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSW 187  
::| | | |:: | | | |:: | | | |:: | | | |:: | | | |  
Db 55 VIGPQ--REEQSPAGPSFNRPLVQTLRSSSQASNNKPAHVAVAN-----ISAP 100

Qy 188 YHDRGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-----ETSGDL 231  
| :| :|| :|| | | | :| :| | | :| :| | | :| :| | | :| :|  
Db 101 GQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFGRHGCPSTPLFLHTISRI 160

Qy 232 ATEYLQIMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISI 291  
| | | | : :|| | :|| | | : | | | | :| :| | :| :|  
Db 161 AVSY-QTKVNIL-SAIKSPCHRETLEGAEAKPW-----YEPIYQGGVFQLEKGDRLSA 211

Qy 292 EVSNPSLLD-PDQDATYFG 309  
|:: | || : |||  
Db 212 EINLPEYLDYAESGGQVYFG 230

#### RESULT 9

QWHUN

tumor necrosis factor alpha precursor [validated] - human

N;Alternate names: cachectin; TNFA

C;Species: Homo sapiens (man)

C;Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Dec-2000

C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23784

R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.; Goeddel, D.V.; Gray, P.W.

Nucleic Acids Res. 13, 6361-6373, 1985

A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chromosomal localization.

A;Reference number: A93585; MUID:86016093; PMID:2995927

A;Accession: A93585

A;Molecule type: DNA

A;Residues: 1-233 <NED>

A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210

R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka, J.; Rodriguez-Tome, P.; Claverie, J.M.; Dausset, J.; Cohen, D. Nature Genet. 3, 137-145, 1993

A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a 90 kilobase HLA class III segment.

A;Reference number: S36152; MUID:93272029; PMID:8499947

A;Accession: S36153

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-233 <IRI>

A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.; Kohr, W.J.; Aggarwal, B.B.; Goeddel, D.V.  
Nature 312, 724-729, 1984  
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to lymphotoxin.  
A;Reference number: A93351; MUID:85086244; PMID:6392892  
A;Accession: A93351  
A;Molecule type: mRNA  
A;Residues: 1-233 <PEN>  
A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelocytic leukemia  
R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Yamamoto, R.; Mark, D.F.  
Science 228, 149-154, 1985  
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
A;Reference number: A44189; MUID:85142190; PMID:3856324  
A;Accession: A44189  
A;Molecule type: mRNA  
A;Residues: 1-62,'S',64-233 <WAN>  
A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738  
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Ando, O.; Torigoe, K.; Sugimoto, T.; Kurimoto, M.  
Lymphokine Res. 7, 175-185, 1988  
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and interferon-alpha from BALL-1 cells stimulated by HVJ.  
A;Reference number: A61478; MUID:88301617; PMID:2841543  
A;Accession: B61478  
A;Molecule type: protein  
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180,'X',182-204 <FUK>  
R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima, E.; Shaw, A.; Johnson, M.  
Eur. J. Biochem. 152, 515-522, 1985  
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison with mouse tumor necrosis factor.  
A;Reference number: I53311; MUID:86030296; PMID:3932069  
A;Accession: I53311  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-233 <MAR>  
A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
A;Experimental source: U-937 cells  
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
Eur. J. Biochem. 235, 431-437, 1996  
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.  
A;Reference number: S62610; MUID:96202967; PMID:8631363  
A;Accession: S62610  
A;Molecule type: protein  
A;Residues: 77-99 <TAK>  
R;D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994  
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter region.  
A;Reference number: I54522; MUID:94102809; PMID:7903959

A;Accession: I54522  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-8 <DAL>  
 A;Cross-references: GB:S68530; NID:g544751  
 R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
 J. Exp. Med. 176, 1053-1062, 1992  
 A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lysine residues.  
 A;Reference number: A59163; MUID:93018820; PMID:1402651  
 A;Contents: annotation; identification of myristylated lysines  
 R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Bringman, T.S.; Nedwin, G.E.; Goeddel, D.V.; Harkins, R.N.  
 J. Biol. Chem. 260, 2345-2354, 1985  
 A;Title: Human tumor necrosis factor. Production, purification, and characterization.  
 A;Reference number: A92511; MUID:85130974; PMID:3871770  
 A;Contents: annotation; disulfide bond  
 C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction, TNF-alpha can cause cytolysis of certain tumor cell lines and have an antiproliferative effect on others without detriment to normal cells. It can also act synergistically with interferon gamma to kill certain transformed cell lines.  
 C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely linked on chromosome 6. They are induced by similar mitogenic stimuli and have similar biological activities but are produced by different cell types and have different induction kinetics.  
 C;Genetics:  
 A;Gene: GDB:TNF; TNFA  
 A;Cross-references: GDB:120441; OMIM:191160  
 A;Map position: 6p21.3-6p21.3  
 A;Introns: 62/3; 78/1; 94/1  
 C;Complex: homotrimer  
 C;Superfamily: tumor necrosis factor  
 C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
 F;1-76/Domain: propeptide #status predicted <PRO>  
 F;77-233/Product: tumor necrosis factor #status experimental <MAT>  
 F;19,20/Binding site: myristate (Lys) (covalent) #status experimental  
 F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental  
 F;145-177/Disulfide bonds: #status experimental

Query Match 7.9%; Score 133; DB 1; Length 233;  
 Best Local Similarity 25.5%; Pred. No. 0.00086;  
 Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

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Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
      :| ||: |   |   ::   | : | | ::| :   : :| | :| :| :
Db      87 KPAHVVAN----PQAEQQL---QWLNRRANALLANGVELRDNQIVVPSEGLYLIYSQVL 139

Qy      222 FRHH--ETSGDLATEYLQIMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273
      |:      :: | | : :   | ||   ::|| |   :| | |   :
Db      140 FKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy      274 SINVGGFKKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
      | :|| | :| | : :| | : : | || :   |||
Db      193 PIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFG 229
  
```

# RESULT 10

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C;Species: Peromyscus leucopus (white-footed mouse)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

C;Accession: I54490

R;Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus (family Cricetidae).

A;Reference number: I54490; MUID:92218012; PMID:1348497

A;Accession: I54490

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-235 <RES>

A;Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C;Genetics:

A;Gene: PlTNF

A;Introns: 62/3; 81/1; 97/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation

F;19,20/Binding site: myristate (Lys) (covalent) #status predicted

F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 7.9%; Score 132.5; DB 2; Length 235;

Best Local Similarity 25.3%; Pred. No. 0.00096;

Matches 42; Conservative 27; Mismatches 54; Indels 43; Gaps 7;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISNMTFSNG-----KLIVNQDGFYYL 216  
:| ||: | :| : || :|| :|:: || | :

Db 90 KPAHVAVN-----HQVDEQLEWLSRG-----ANALLANGMDLKDNLVIPADGLYLV 137

Qy 217 YANICFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYW 264  
|: : |: | : |: | |: :|| | :| | |

Db 138 YSQVLFK-----GQGCSSYVLLTHTVSRFAVSIEDKVNLLSAIKSPCKETPEGSELKPW 192

Qy 265 SGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD-PDQDATYFG 309  
: | :|| |:| |: :| ||: | || : |||

Db 193 -----YEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFG 231

# RESULT 11

JU0029

tumor necrosis factor alpha precursor - rat

N;Alternate names: cachectin; TNF alpha

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Feb-2000

C;Accession: JU0029; JN0868; S21674

R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.

Agric. Biol. Chem. 53, 1733-1736, 1989

A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor.

A;Reference number: JU0029

A;Accession: JU0029

A;Molecule type: DNA

A;Residues: 1-235 <SHI>  
 R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.  
 Gene 132, 227-236, 1993  
 A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.  
 A;Reference number: JN0868; MUID:94040766; PMID:8224868  
 A;Accession: JN0868  
 A;Molecule type: DNA  
 A;Residues: 1-235 <KWO>  
 A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254  
 R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.  
 Biol. Chem. Hoppe-Seyler 373, 271-281, 1992  
 A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro posttranslational processing based on a PCR-derived cDNA.  
 A;Reference number: S21674; MUID:92329007; PMID:1627266  
 A;Accession: S21674  
 A;Molecule type: mRNA  
 A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>  
 A;Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370  
 C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and produces hemorrhagic necrosis of tumors.  
 C;Genetics:  
 A;Gene: TNF-alpha  
 A;Introns: 62/3; 81/1; 97/1  
 C;Superfamily: tumor necrosis factor  
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane protein; myristylation  
 F;80-235/Product: tumor necrosis factor #status predicted <MAT>  
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;148-179/Disulfide bonds: #status predicted

Query Match 7.8%; Score 131.5; DB 2; Length 235;  
 Best Local Similarity 25.3%; Pred. No. 0.0012;  
 Matches 41; Conservative 27; Mismatches 59; Indels 35; Gaps 7;

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Qy      163 QPFAHLTINATDIPSGSHKVSLS--SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
          :| ||: |           |:         | | | :| | : :| | || | :| :
Db      90 KPAHVAVN-----HQAEEQLEWLSQRANALLANGMDLKDNLVVPADGLYLIYSQV 141

Qy      221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268
          |:      |      :|: |      |::          :|| |      :| | |
Db      142 LFK-----GQGCPDYVLLTHTVSRFAISYQEKVSLLSAIKSPCPKDTPEGAELKPW----- 192

Qy      269 EFHFYSINVGGFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
          : : || |:| |: :| ||: | || :   |||
Db      193 ---YEPMYLGGVFQLEKGDLLSAEVNLPKYLDITESGQVYFG 231

```

RESULT 12

I49139

lymphotoxin-beta - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I49139; I49138; I49076





C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
 C;Accession: S22052  
 R;Sanjanwala, M.; Edwards, A.  
 submitted to the EMBL Data Library, September 1991  
 A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.  
 A;Reference number: S22052  
 A;Accession: S22052  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-233 <SAN>  
 A;Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160  
 C;Genetics:  
 A;Introns: 62/3; 78/1; 94/1  
 C;Superfamily: tumor necrosis factor  
 C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein  
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F;145-177/Disulfide bonds: #status predicted

Query Match 7.7%; Score 130; DB 1; Length 233;  
 Best Local Similarity 25.5%; Pred. No. 0.0015;  
 Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

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Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
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Db      87 KPAHVVAN----PQAEQQL---QWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVL 139

Qy      222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273
          |:  ::  || :  :  ||  ::|| |  :|  ||  :
Db      140 FKGQGPCSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 192

Qy      274 SINVGGFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
          | :|| |:| |: :| |: : | || :  |||
Db      193 PIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFG 229
  
```

#### RESULT 14

JQ1344

tumor necrosis factor alpha precursor - horse

N;Alternate names: cachectin; TNF alpha

C;Species: Equus caballus (domestic horse)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C;Accession: JQ1344

R;Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor alpha.

A;Reference number: JQ1344; MUID:92084125; PMID:1748301

A;Accession: JQ1344

A;Molecule type: DNA

A;Residues: 1-234 <SUX>

A;Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C;Comment: This protein is an important proximal mediator of endotoxemia.

C;Genetics:

A;Gene: TNF-alpha

A;Introns: 62/3; 79/1; 95/1

C;Superfamily: tumor necrosis factor  
 C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine;  
 macrophage; membrane protein; myristylation  
 F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
 F;19,20/Binding site: myristate (Lys) (covalent) #status predicted  
 F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F;146-178/Disulfide bonds: #status predicted

Query Match 7.6%; Score 128; DB 1; Length 234;  
 Best Local Similarity 24.2%; Pred. No. 0.0023;  
 Matches 39; Conservative 32; Mismatches 58; Indels 32; Gaps 8;

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Qy      163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
          :| ||: |   |   :: |   | | :| : :: :| | | :| :
Db      88 KPVAHVVAN-----PQAEQQL---QWLSGRANALLANGVKLTDNQLVVPLDGLYLIYSQVL 140

Qy      222 FRHHETSGDLATEYQLMVVYTKTSIKIPSSHTLMKG-----GSTKYWSGNSE 269
          | :   | :| | |   :: :| | | :   | |   | |
Db      141 FK---GQGCPSTHVL-LTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPW----- 191

Qy      270 FHFYSINVGGFKKLSRGEEISIEVSNPSLLD-PDQDATYFG 309
          : | :|| | :| | :|| | :| :| : | | :   |||
Db      192 --YEPIYLGGVFQLEKGDQLSAEINQPNYLDFAESGQVYFG 230
  
```

# RESULT 15

S24642

tumor necrosis factor alpha precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C;Accession: I46047; S24642

R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tumour necrosis factor-alpha genes.

A;Reference number: I46046; MUID:94083525; PMID:8260599

A;Accession: I46047

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-233 <CL2>

A;Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C;Genetics:

A;Gene: TNFA

A;Introns: 62/3; 78/1; 94/1

C;Superfamily: tumor necrosis factor

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;20/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 7.5%; Score 126.5; DB 1; Length 233;  
 Best Local Similarity 25.5%; Pred. No. 0.0031;  
 Matches 50; Conservative 25; Mismatches 80; Indels 41; Gaps 9;

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Qy      134 IVGSQHIRAEKAMVDGSWLDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSWYHD 190
          ::| | :   | |   || :| :| ||:   || |
Db      55 VIGPQREESPGGPSINSPLVQTLRSSSQASSNKPVAHV---VADINSPGQL----- 102
  
```

Qy 191 RGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-----ETSGDLATE 234  
 | | :| :|| :|| | | :|: : || | :|  
 Db 103 RWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFRGQGCPSTPLFLHTISRIAVS 162  
  
 Qy 235 YLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVS 294  
 | | | : :|| | : | | : | || | : | | : | | :  
 Db 163 Y-QTKVNIL-SAIKSPCHRETPEWAEAKPW-----YEPIYQGGVFQLEKGDRLSAEIN 213  
  
 Qy 295 NPSLLD-PDQDATYFG 309  
 | || : |||  
 Db 214 LPDYLDYAESGQVYFG 229

Search completed: February 25, 2004, 16:31:07  
 Job time : 31 secs

OM protein - protein search, using sw model

Run on: February 25, 2004, 16:30:32 ; Search time 36 Seconds  
(without alignments)  
1859.322 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							

1	1685	100.0	317	9	US-09-813-329-7	Sequence 7, Appli
2	1685	100.0	317	9	US-09-871-856-13	Sequence 13, Appl
3	1685	100.0	317	9	US-09-877-650-13	Sequence 13, Appl
4	1685	100.0	317	14	US-10-218-547-22	Sequence 22, Appl
5	1685	100.0	317	14	US-10-405-878-13	Sequence 13, Appl
6	1685	100.0	317	14	US-10-167-182-11	Sequence 11, Appl
7	1685	100.0	317	14	US-10-310-793-28	Sequence 28, Appl
8	1685	100.0	317	15	US-10-460-623-11	Sequence 11, Appl
9	1417.5	84.1	316	10	US-09-079-569-7	Sequence 7, Appli
10	1417.5	84.1	316	10	US-09-873-829-4	Sequence 4, Appli
11	1417.5	84.1	316	13	US-10-017-910-4	Sequence 4, Appli
12	1417.5	84.1	316	14	US-10-105-057-2	Sequence 2, Appli
13	1417.5	84.1	316	14	US-10-272-411-19	Sequence 19, Appl
14	1417.5	84.1	316	14	US-10-272-328A-19	Sequence 19, Appl
15	1417.5	84.1	316	14	US-10-326-052-2	Sequence 2, Appli
16	1417.5	84.1	316	14	US-10-167-182-1	Sequence 1, Appli
17	1417.5	84.1	316	15	US-10-460-623-1	Sequence 1, Appli
18	1326.5	78.7	294	9	US-09-871-856-11	Sequence 11, Appl
19	1326.5	78.7	294	9	US-09-877-650-11	Sequence 11, Appl
20	1326.5	78.7	294	14	US-10-405-878-11	Sequence 11, Appl
21	1325	78.6	250	15	US-10-338-785A-1	Sequence 1, Appli
22	1319	78.3	249	14	US-10-050-902-221	Sequence 221, App
23	1319	78.3	249	14	US-10-050-898-221	Sequence 221, App
24	1301	77.2	246	14	US-10-167-182-17	Sequence 17, Appl
25	1301	77.2	246	15	US-10-460-623-17	Sequence 17, Appl
26	1293	76.7	245	10	US-09-873-829-2	Sequence 2, Appli
27	1293	76.7	245	13	US-10-017-910-2	Sequence 2, Appli
28	1292	76.7	244	14	US-10-210-951-42	Sequence 42, Appl
29	1292	76.7	244	14	US-10-050-902-222	Sequence 222, App
30	1292	76.7	244	14	US-10-050-898-222	Sequence 222, App
31	1292	76.7	244	14	US-10-211-884-42	Sequence 42, Appl
32	1133	67.2	249	15	US-10-338-785A-3	Sequence 3, Appli
33	1127	66.9	247	14	US-10-050-902-223	Sequence 223, App
34	1127	66.9	247	14	US-10-050-898-223	Sequence 223, App
35	1109	65.8	244	14	US-10-167-182-16	Sequence 16, Appl
36	1109	65.8	244	15	US-10-460-623-16	Sequence 16, Appl
37	962	57.1	185	14	US-10-050-902-320	Sequence 320, App
38	962	57.1	185	14	US-10-050-898-320	Sequence 320, App
39	909	53.9	199	14	US-10-050-902-224	Sequence 224, App
40	909	53.9	199	14	US-10-050-898-224	Sequence 224, App
41	852	50.6	160	9	US-09-779-050A-15	Sequence 15, Appl
42	848	50.3	178	15	US-10-338-785A-2	Sequence 2, Appli
43	825	49.0	419	14	US-10-050-902-318	Sequence 318, App
44	825	49.0	419	14	US-10-050-898-318	Sequence 318, App
45	809	48.0	151	14	US-10-338-083-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1  
 US-09-813-329-7  
 ; Sequence 7, Application US/09813329  
 ; Patent No. US20020012968A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Suibb Company

; TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor  
 Class Molecule ("DmTNF") and  
 ; TITLE OF INVENTION: Variants Thereof  
 ; FILE REFERENCE: D0016.np  
 ; CURRENT APPLICATION NUMBER: US/09/813,329  
 ; CURRENT FILING DATE: 2001-03-20  
 ; PRIOR APPLICATION NUMBER: 60/190,816  
 ; PRIOR FILING DATE: 2000-03-21  
 ; NUMBER OF SEQ ID NOS: 65  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 317  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-813-329-7

Query Match 100.0%; Score 1685; DB 9; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-156;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
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 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
  
 QY 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
 QY 121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 QAFQGA VQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
  
 QY 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQIMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQIMV 240  
  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGE EISIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGE EISIEVSNPSLLD 300  
  
 QY 301 PDQDATYFGAFKVRDID 317  
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 Db 301 PDQDATYFGAFKVRDID 317

RESULT 2

US-09-871-856-13

; Sequence 13, Application US/09871856  
 ; Patent No. US20020081720A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Dirk M.  
 ; Galibert, Laurent  
 ; Maraskovsky, Eugene  
 ; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation, Law Department

```

; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
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; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

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Query Match          100.0%; Score 1685; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 9.4e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
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Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240

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Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 |||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 Qy 301 PDQDATYFGAFKVRDID 317  
 |||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 3

US-09-877-650-13

; Sequence 13, Application US/09877650

; Patent No. US20020169117A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/877,650

; FILING DATE: 08-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/995,659

; FILING DATE: 1997-12-22

; APPLICATION NUMBER: USSN 08/813,509

; FILING DATE: 07 MARCH 1997

; APPLICATION NUMBER: USSN 08/772,330

; FILING DATE: 23 DECEMBER 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Perkins, Patricia Anne

; REGISTRATION NUMBER: 34,693

; REFERENCE/DOCKET NUMBER: 2852-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430

; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 317 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-877-650-13



Query Match 100.0%; Score 1685; DB 9; Length 317;  
Best Local Similarity 100.0%; Pred. No. 9.4e-156;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQIMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQIMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
        ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317
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RESULT 4

US-10-218-547-22

; Sequence 22, Application US/10218547

; Publication No. US20030100074A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Relating To

; TITLE OF INVENTION: Human Endokine Alpha

; FILE REFERENCE: PF561

; CURRENT APPLICATION NUMBER: US/10/218,547

; CURRENT FILING DATE: 2002-08-15

; PRIOR APPLICATION NUMBER: 60/312,542

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/330,761

; PRIOR FILING DATE: 2001-10-30

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 22

; LENGTH: 317

; TYPE: PRT

; ORGANISM: human

US-10-218-547-22

Query Match 100.0%; Score 1685; DB 14; Length 317;  
Best Local Similarity 100.0%; Pred. No. 9.4e-156;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 |||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 |||||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240  
 |||||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300  
 |||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRS GEEISIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 |||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 5

US-10-405-878-13

; Sequence 13, Application US/10405878

; Publication No. US20030175840A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, Dirk M.

; Galibert, Laurent

; Maraskovsky, Eugene

; TITLE OF INVENTION: Receptor Activator of NF-kappaB

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation, Law Department

; STREET: 51 University Street

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Power Macintosh

; OPERATING SYSTEM: Apple Operating System 7.5.5

; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/405,878

; FILING DATE: 01-Apr-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/996,139

; FILING DATE: 22 DECEMBER 1997

; APPLICATION NUMBER: USSN 60/064,671

; FILING DATE: 14 OCTOBER 1997

; APPLICATION NUMBER: USSN 08/813,509  
 ; FILING DATE: 07 MARCH 1997  
 ; APPLICATION NUMBER: USSN 08/772,330  
 ; FILING DATE: 23 DECEMBER 1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia Anne  
 ; REGISTRATION NUMBER: 34,693  
 ; REFERENCE/DOCKET NUMBER: 2851-A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206)587-0430  
 ; TELEFAX: (206)233-0644  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 317 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-10-405-878-13

Query Match 100.0%; Score 1685; DB 14; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-156;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60  
 |||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 |||||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 Qy 181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 |||||  
 Db 181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240  
 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300  
 |||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLD 300  
 Qy 301 PDQDATYFGAFKVRDID 317  
 |||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 6

US-10-167-182-11

; Sequence 11, Application US/10167182  
 ; Publication No. US20030176647A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yamaguchi, Kyoji  
 ; APPLICANT: Yasuda, Hisataka  
 ; APPLICANT: Nakagawa, No. US20030176647Aluaki

```

; APPLICANT: Shima, No. US20030176647A1uyuki
; APPLICANT: Kinoshita, Masahiko
; APPLICANT: Tsuda, Eisuke
; APPLICANT: Goto, Masaaki
; APPLICANT: Yano, Kazuki
; APPLICANT: Tomoyasu, Akihiro
; APPLICANT: Kobayashi, Fumie
; APPLICANT: Washida, Naohiro
; APPLICANT: Takahashi, Ken
; APPLICANT: Morinaga, Tomonori
; APPLICANT: Higashio, Kanji
; TITLE OF INVENTION: Antibodies to OCIF-binding Molecules
; FILE REFERENCE: FJN-070DV
; CURRENT APPLICATION NUMBER: US/10/167,182
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 09/202,455
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: JP 97808/1997
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: JP 151434/1997
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: JP 217897/1997
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: JP 224803/1997
; PRIOR FILING DATE: 1997-08-21
; PRIOR APPLICATION NUMBER: JP 332241/1997
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-182-11

```

```

Query Match          100.0%; Score 1685; DB 14; Length 317;
Best Local Similarity 100.0%; Pred. No. 9.4e-156;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQMV 240

```

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300  
 Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 7

US-10-310-793-28

; Sequence 28, Application US/10310793

; Publication No. US20030198640A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ni, Jian

; APPLICANT: Rosen, Craig A

; APPLICANT: Zhang, Jun

; APPLICANT: Wei, Ping

; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases

; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta

; FILE REFERENCE: PF573

; CURRENT APPLICATION NUMBER: US/10/310,793

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: 60/336,695

; PRIOR FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: 10/226,294

; PRIOR FILING DATE: 2002-08-23

; PRIOR APPLICATION NUMBER: 60/314,381

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 09/899,059

; PRIOR FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: 60/278,449

; PRIOR FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: 60/216,879

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: 09/559,290

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/180,908

; PRIOR FILING DATE: 2000-02-08

; PRIOR APPLICATION NUMBER: 60/134,067

; PRIOR FILING DATE: 1999-05-13

; PRIOR APPLICATION NUMBER: 60/132,227

; PRIOR FILING DATE: 1999-05-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 28

; LENGTH: 317

; TYPE: PRT

; ORGANISM: human

US-10-310-793-28

Query Match 100.0%; Score 1685; DB 14; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-156;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60  
 |||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 |||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180  
 |||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240  
 |||  
 Db 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240

Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300  
 |||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESIEVSNPSLLD 300

Qy 301 PDQDATYFGAFKVRDID 317  
 |||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 8

US-10-460-623-11

; Sequence 11, Application US/10460623

; Publication No. US20030208045A1

; GENERAL INFORMATION:

; APPLICANT: Yamaguchi, Kyoji

; APPLICANT: Yasuda, Hisataka

; APPLICANT: Nakagawa, No. US20030208045A1uaki

; APPLICANT: Shima, No. US20030208045A1uyuki

; APPLICANT: Kinosaki, Masahiko

; APPLICANT: Tsuda, Eisuke

; APPLICANT: Goto, Masaaki

; APPLICANT: Yano, Kazuki

; APPLICANT: Tomoyasu, Akihiro

; APPLICANT: Kobayashi, Fumie

; APPLICANT: Washida, Naohiro

; APPLICANT: Takahashi, Ken

; APPLICANT: Morinaga, Tomonori

; APPLICANT: Higashio, Kanji

; TITLE OF INVENTION: No. US20030208045A1el Protein and Method for Producing the Protein

; FILE REFERENCE: FJN-070

; CURRENT APPLICATION NUMBER: US/10/460,623

; CURRENT FILING DATE: 2003-06-13

; PRIOR APPLICATION NUMBER: JP 97808/1997

; PRIOR FILING DATE: 1997-04-15

; PRIOR APPLICATION NUMBER: JP 151434/1997

; PRIOR FILING DATE: 1997-06-09

; PRIOR APPLICATION NUMBER: JP 217897/1997

; PRIOR FILING DATE: 1997-08-12

; PRIOR APPLICATION NUMBER: JP 224803/1997

; PRIOR FILING DATE: 1997-08-21  
 ; PRIOR APPLICATION NUMBER: JP 332241/1997  
 ; PRIOR FILING DATE: 1997-12-02  
 ; PRIOR APPLICATION NUMBER: WO PCT/JP98/01728  
 ; PRIOR FILING DATE: 1998-04-15  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 317  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-460-623-11

Query Match 100.0%; Score 1685; DB 15; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-156;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60  
  
 Qy 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
  
 Qy 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
  
 Qy 181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 KVSLSWYHNRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240  
  
 Qy 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEESIEVSNPSLLD 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEESIEVSNPSLLD 300  
  
 Qy 301 PDQDATYFGAFKVRDID 317  
 ||||||||||||||||  
 Db 301 PDQDATYFGAFKVRDID 317

RESULT 9

US-09-079-569-7

; Sequence 7, Application US/09079569  
 ; Publication No. US20030104485A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boyle, William J.  
 ; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Amgen Inc.  
 ; STREET: 1840 Dehavilland Drive  
 ; CITY: Thousand Oaks  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 91230-1789

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,569
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/842,842
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-079-569-7

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Query Match          84.1%; Score 1417.5; DB 10; Length 316;
Best Local Similarity 84.3%; Pred. No. 1.1e-129;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

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Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59
        ||||| ||| |||| ||| ||||| || ||| |||||:|||||
Db      1 MRRASRDYGKYLRSEEMGSGGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy     60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
        |||:| ||||| ||||| ||| ||||| ||| ||:||||:| :||||:
Db     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRMM 118

Qy    120 KQAFQGA VQKELQHIVGSGHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGS 179
        ||||| ||||| ||| ||:||||:| ||| ||||| |||||
Db    119 KQAFQGA VQKELQHIVGPGRFSGAPAMMEGSWLDVAQRGKPEAQPF AHLTINAASIPSGS 178

Qy    180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
        |||:||||| ||||| ||||| ||||| ||||| ||||| :|:||||
Db    179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy    240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLL 299
        ||| ||||| ||||| ||||| ||||| ||||| ||||| :||||:|||||
Db    239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVG GFFKL RAGEEISIQVSNPSLL 298

Qy    300 DPDQDATYFGAFKVRDID 317
        ||||| ||||| |||||
Db    299 DPDQDATYFGAFKVQDID 316

```

RESULT 10

US-09-873-829-4

; Sequence 4, Application US/09873829

; Publication No. US20030185820A1

; GENERAL INFORMATION:



```

;      APPLICANT: Choi, Yongwon
;              Wong, Brian
;              Josien, Regis
;              Steinman, Ralph
;      TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF  SUPERFAMILY
;                          INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS
ENCODING SAME, AND
;                          METHODS OF USE THEREOF
;
;      NUMBER OF SEQUENCES: 18
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Klauber & Jackson
;          STREET: 411 Hackensack Avenue, 4th Floor
;          CITY: Hackensack
;          STATE: New Jersey
;          COUNTRY: USA
;          ZIP: 07601
;
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/873,829
;          FILING DATE: 04-Jun-2001
;          CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 09/210,115
;          FILING DATE: <Unknown>
;
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Jackson Esq., David A.
;          REGISTRATION NUMBER: 26,742
;          REFERENCE/DOCKET NUMBER: 600-1-200 CIP N
;
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 201-487-5800
;          TELEFAX: 201-343-1684
;          TELEX: 133521
;
;      INFORMATION FOR SEQ ID NO: 4:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 316 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-873-829-4

```

```

Query Match          84.1%;  Score 1417.5;  DB 10;  Length 316;
Best Local Similarity 84.3%;  Pred. No. 1.1e-129;
Matches 268;  Conservative 16;  Mismatches 31;  Indels 3;  Gaps 2;

```

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHQPPAASRSMFVALLGLGLGQ 59
        ||||| ||| |||| ||| ||||| || ||| |||||:|||||
Db      1 MRRASRDYGKYLRSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy      60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
        |||:||| ||||| ||||| ||| ||||| ||| |||:||| :|||:
Db      61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRRM 118

```

TELEFAX: 201-343-1684

; TELEX: 133521  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 316 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-10-017-910-4

Query Match 84.1%; Score 1417.5; DB 13; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 1.1e-129;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ 59  
 ||||| ||| |||| ||| ||||| || ||| |||||:|||||  
 Db 1 MRRASRDYGKYLRSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60  
 Qy 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119  
 |||:||| ||||| ||| ||||| ||:||||:| :|||:  
 Db 61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRMM 118  
 Qy 120 KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFahlTINATDIPSGS 179  
 ||||| ||||| ||| ||:||||:| || ||||| |||||  
 Db 119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFahlTINAASIPSGS 178  
 Qy 180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIM 239  
 |||:||||| ||||| ||||| ||||| ||||| :|:||||  
 Db 179 HKVTLSSWYHDRGWAKISNMTLSNGKLIRVNQDGFYYLYANICFRHHETSGSVPTDYLQIM 238  
 Qy 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSSL 299  
 ||| ||||| ||||| ||||| ||||| |||||:||||:|||||  
 Db 239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGFFKLRAGEEISIQVSNPSSL 298  
 Qy 300 DPDQDATYFGAFKVRDID 317  
 ||||| |||||  
 Db 299 DPDQDATYFGAFKVQDID 316

# RESULT 12

US-10-105-057-2

; Sequence 2, Application US/10105057  
 ; Publication No. US20030013651A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barnes-Jewish Hospital, d/b/a The Jewish Hospital of St. Louis  
 ; TITLE OF INVENTION: STIMULATION OF OSTEOGENESIS USING RANK LIGAND FUSION  
 PROTEINS  
 ; FILE REFERENCE: BJCH 10054.1  
 ; CURRENT APPLICATION NUMBER: US/10/105,057  
 ; CURRENT FILING DATE: 2002-03-22  
 ; PRIOR APPLICATION NUMBER: US 60/277,855  
 ; PRIOR FILING DATE: 2001-03-22  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 316  
 ; TYPE: PRT

; ORGANISM: Mus musculus  
US-10-105-057-2

Query Match 84.1%; Score 1417.5; DB 14; Length 316;  
Best Local Similarity 84.3%; Pred. No. 1.1e-129;  
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

```
Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59
        ||||| |||| |||| ||| ||||| || ||| |||||:|||||
Db      1 MRRASRDYGKYLRSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy     60 VVCSVALLFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
        |||:||| ||||| ||||| ||| ||||| ||| ||:||||:| :|||||:
Db     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRMM 118

Qy    120 KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPSGS 179
        ||||| ||||| ||| |||:||||:|:| ||||| |||||
Db    119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPF AHLTINAASIPSGS 178

Qy    180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQM 239
        |||:||||| ||||| ||||| ||||| ||||| ||||| :|:||||
Db    179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy    240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPSLL 299
        ||| ||||| ||||| ||||| ||||| ||||| |||||:|||||:|||||
Db    239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRSAGEEISIQVSNPSLL 298

Qy    300 DPDQDATYFGAFKVRDID 317
        ||||| |||||:|||
Db    299 DPDQDATYFGAFKVQDID 316
```

RESULT 13

US-10-272-411-19

; Sequence 19, Application US/10272411  
; Publication No. US20030100068A1  
; GENERAL INFORMATION:  
; APPLICANT: Barnes Jewish Hospital  
; APPLICANT: Lam, Jonathan  
; APPLICANT: Ross, F. Patrick  
; APPLICANT: Teitelbaum, Steven  
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF  
; FILE REFERENCE: 60019620-0202  
; CURRENT APPLICATION NUMBER: US/10/272,411  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/329,393  
; PRIOR FILING DATE: 2001-10-15  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-411-19

Query Match 84.1%; Score 1417.5; DB 14; Length 316;  
Best Local Similarity 84.3%; Pred. No. 1.1e-129;

Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59
        ||||| |||| |||| ||| ||||| || ||| |||||:|||||
Db      1 MRRASRDYGKYLRSSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy     60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
        |||:||| ||||| ||||| ||| ||||| ||| ||:||||:| :|||:|
Db     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRMM 118

Qy    120 KQAFQGAVQKELQHIVGSGHRAEKAMVDGSWLDLAKRSKLEAQPFPAHLTINATDIPSGS 179
        ||||| ||||| ||||| ||| ||:||||:|:| ||||| |||||
Db    119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFPAHLTINAASIPSGS 178

Qy    180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYQLQM 239
        |||:||||| ||||| ||||| ||||| ||||| ||||| :|:||||
Db    179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy    240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEIEISIEVSNPSLL 299
        ||| ||||| ||||| ||||| ||||| ||||| |||||:||||:|
Db    239 VYVVKTSIKIPSSSHNLMKGGSTKNWSGNSEFHFYSINVGFFKLRSAGEEISIQVSNPSLL 298

Qy    300 DPDQDATYFGAFKVRDID 317
        ||||| ||||| |||||
Db    299 DPDQDATYFGAFKVQDID 316

```

# RESULT 14

US-10-272-328A-19

```

; Sequence 19, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-328A-19

```

Query Match 84.1%; Score 1417.5; DB 14; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 1.1e-129;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59
        ||||| |||| |||| ||| ||||| || ||| |||||:|||||
Db      1 MRRASRDYGKYLRSSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

```

Qy	60	VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFDQDTTLESQDTKLIPDSCRRI	119
Db	61	VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRRM	118
Qy	120	KQAFQGA>VQKELQHIVGSQHIRAEKAMVDG>SWLDLAKRSKLEAQPFAHLTINATDIPSGS	179
Db	119	KQAFQGA>VQKELQHIVGPQRFSGAPAMMEG>SWLDVAQRGKPEAQPFAHLTINAASIPSGS	178
Qy	180	HKVSLSSWYHDRGWAKISNM>TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM	239
Db	179	HKVTLSSWYHDRGWAKISNM>TLSNGKLVRNQDGFYYLYANICFRHHETSGSVPTDYLQLM	238
Qy	240	VYVTKTSIKIPSSHTLMKGGSTKYWSGNSE>FHFYSINVG>GF>FKLRSGEEISIEVSNPSLL	299
Db	239	VYVVKTSIKIPSSHNLMKGGSTKNWSGNSE>FHFYSINVG>GF>FKLRAGEEISIQVSNPSLL	298
Qy	300	DPDQDATYFGAFKVRDID	317
Db	299	DPDQDATYFGAFKVQDID	316

```

;      REGISTRATION NUMBER: 34,090
;      REFERENCE/DOCKET NUMBER: DX0686
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (650)852-9196
;      TELEFAX: (650)496-1204
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 316 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-326-052-2

```

```

Query Match      84.1%; Score 1417.5; DB 14; Length 316;
Best Local Similarity 84.3%; Pred. No. 1.1e-129;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

```

```

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ 59
        ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      1 MRRASRDYGKYLRSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ 60

Qy      60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
        ||||:|||| ||||| ||||| |||| ||||| |||| ||||| ||||| |||||:
Db      61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESED--LPDSCRMM 118

Qy      120 KQAFQGAVQKELQHIVGVSQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGS 179
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFHAHLTINAASIPSGS 178

Qy      180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
        ||||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      179 HKVTLSSWYHDRGWAKISNMTLSNGKLIVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238

Qy      240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLAGEEISIQVSNPSLL 298

Qy      300 DPDQDATYFGAFKVRDID 317
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      299 DPDQDATYFGAFKVQDID 316

```

```

Search completed: February 25, 2004, 16:36:10
Job time : 38 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2004, 16:25:23 ; Search time 46 Seconds  
(without alignments)  
2174.332 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaphage:\*  
17: sp\_archaeophages:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description
<hr/>		



1	266	15.8	317	13	Q7ZYX9	Q7zyx9 brachydanio
2	265	15.7	304	13	Q7T1F2	Q7t1f2 gallus gall
3	240.5	14.3	214	13	Q9DDZ5	Q9ddz5 brachydanio
4	216.5	12.8	287	13	Q90WT9	Q90wt9 gallus gall
5	215.5	12.8	287	11	Q8K3G0	Q8k3g0 rattus norv
6	194.5	11.5	280	6	Q861W5	Q861w5 felis silve
7	187.5	11.1	279	11	Q7TMV9	Q7tmv9 mus musculu
8	184.5	10.9	252	11	Q8K3Y8	Q8k3y8 mus musculu
9	179.5	10.7	252	11	Q80YZ0	Q80yz0 mus musculu
10	177.5	10.5	252	11	Q8K3Y7	Q8k3y7 rattus norv
11	156.5	9.3	251	4	Q8NFE9	Q8nfe9 homo sapien
12	139.5	8.3	215	11	Q99ND1	Q99nd1 tamiasciuru
13	137.5	8.2	156	11	Q91ZL4	Q91zl4 sigmodon hi
14	137.5	8.2	232	11	Q80XA4	Q80xa4 peromyscus
15	133	7.9	149	6	O97543	O97543 aotus nancy
16	131.5	7.8	216	11	O70332	O70332 mesocricetu
17	130	7.7	217	11	Q9ERG6	Q9erg6 peromyscus
18	127.5	7.6	217	6	Q9BEC5	Q9bec5 tenrec ecau
19	126	7.5	149	6	O97538	O97538 aotus vocif
20	126	7.5	149	6	Q9TTG8	Q9ttg8 aotus nigri
21	126	7.5	302	11	Q7TSL5	Q7tsl5 peromyscus
22	125	7.4	216	6	Q9BEC9	Q9bec9 ochotona pr
23	120.5	7.2	217	6	Q9BEG0	Q9beg0 cyclopes di
24	120.5	7.2	217	6	Q9BEG1	Q9beg1 bradypus tr
25	118.5	7.0	138	6	Q9TTG7	Q9ttg7 aotus lemur
26	117	6.9	244	6	Q862Z7	Q862z7 pan troglod
27	116.5	6.9	169	11	Q9WV90	Q9wv90 marmota mon
28	115.5	6.9	154	6	Q8MJ19	Q8mj19 macaca mula
29	114.5	6.8	216	6	Q9BEE0	Q9bee0 macropus ru
30	113.5	6.7	216	6	Q9BEC4	Q9bec4 talpa europ
31	113.5	6.7	237	13	Q8AWC9	Q8awc9 cyprinus ca
32	113	6.7	217	6	Q9BEF4	Q9bef4 cabassous u
33	111	6.6	102	11	Q80Z03	Q80z03 castor cana
34	110.5	6.6	215	6	Q9BEE8	Q9bee8 erinaceus e
35	110	6.5	102	11	Q80Z02	Q80z02 trichys fas
36	109.5	6.5	253	13	Q7T194	Q7t194 acanthopagr
37	109	6.5	102	11	Q80Z05	Q80z05 dipodomys m
38	108	6.4	102	11	Q80Z06	Q80z06 dipus sagit
39	107.5	6.4	222	13	Q7T1U4	Q7t1u4 pagrus majo
40	107.5	6.4	409	5	Q8MY88	Q8my88 drosophila
41	107.5	6.4	409	5	Q8IGD3	Q8igd3 drosophila
42	106.5	6.3	325	5	Q9V5G2	Q9v5g2 drosophila
43	106.5	6.3	415	5	Q8MUJ1	Q8muj1 drosophila
44	106	6.3	3467	5	Q8I218	Q8i218 plasmodium
45	105.5	6.3	103	6	Q864Z0	Q864z0 physeter ca

#### ALIGNMENTS

##### RESULT 1

Q7ZYX9

ID Q7ZYX9 PRELIMINARY; PRT; 317 AA.

AC Q7ZYX9;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Similar to tumor necrosis factor (Ligand) superfamily, member 10.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC044336; AAH44336.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCE9F CRC64;

Query Match 15.8%; Score 266; DB 13; Length 317;  
 Best Local Similarity 26.6%; Pred. No. 1.4e-15;  
 Matches 79; Conservative 66; Mismatches 122; Indels 30; Gaps 9;

Qy 42 PAASR-----SMFVALLGLGLG--QVCSVALFFYFRAQMDPNRISEDGTHCIYRILRL 93  
 || || ::||: : : | : : || | | : : | | |  
 Db 24 PANSRGRDSPSKLWIAMVIVVVVLQIASTTGLFVYL--NMSLSQVKSQGVTEELRCLGL 81  
 Qy 94 HENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQKELQHIVGSQHIRAEKAMVDGSWLD 153  
 | :| : :| :| : : : :| | :| :| :  
 Db 82 -LNVLGKDQDIPEDLAQLFGPECMKLAEGIKAYISKVTDSIISKQTLHAARTRTHSYNTT 140  
 Qy 154 LAK-RSKLEAQPFHAHLTINATDIPS-----GSHKVSLSWYHDRGWAKISN 198  
 :| : : :| ||| : : | : : :| : :| :|  
 Db 141 GSKFMTTVMQRPSAHLTLSSASDNSRPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLN 200  
 Qy 199 MTFSGNKLIVNQDGFYYLYANICFRHHETS-GDLATEYLQIMVYV-TKTSIKIPSSHTLM 256  
 || :||:| | ||| ||| : : ||: | | : : ||: : ||| | :  
 Db 201 MTLTNGRLRVPQDGRYYLYSQVYFRYPSPSDSDQSSVSHQLVQCIYKKTSYLNPIQ--LL 258  
 Qy 257 KGGSTKYWSGNSEFHFYSINVGGFKLRSGEIEISIEVSNPSLLDPDQDATYFGAFKV 313  
 || || | : :||: :|| || :||:| : : ||:| : : : :||| : :  
 Db 259 KGVGTKCWAPDAEYALHSVYQGGLFELRAGDEVFVSVSPTMVYGEDSSSYFGAFRL 315

## RESULT 2

Q7T1F2

ID Q7T1F2 PRELIMINARY; PRT; 304 AA.  
 AC Q7T1F2;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor related apoptosis inducing ligand.  
 GN TRAIL.

OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Sayed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;  
 RT "Identification and Characterization of Chicken TNF-Superfamily  
 RT Ligand 8 (CD30 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis  
 RT Inducing Ligand TRAIL).";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB114678; BAC79267.1; -.  
 SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 15.7%; Score 265; DB 13; Length 304;  
 Best Local Similarity 27.3%; Pred. No. 1.6e-15;  
 Matches 82; Conservative 56; Mismatches 126; Indels 36; Gaps 12;

Qy 38 PHQPPAASRSMFVALLGLGLGQVVCVAFYFRAQMDP--NRISEDGTHCI--YRILRL 93  
 | | : : : | : | | | : | | : : | | | : : |  
 Db 3 PAGGPSPAHTCGAVLVAAVLLQSVCAVYIYFTNELKQLWDTYSRSGTACLTGEELGDL 62  
 Qy 94 HENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQKELQHIVGSQHIRAEKAMVDGSWLD 153  
 : | | : | | : | | : | : | : | : : : : : |  
 Db 63 IQNLD----VVESKDR--VADPCWQVKWHLGKLIKMMMSRI-----LQENMSAINGDRTQ 111  
 Qy 154 -LAKRSKLEAQP----FAHLTINATDIPSGSHKV-----SLSSWYHD-RGWAKISNM 199  
 | : | : | | | | : : : | : | | : : | : : | :  
 Db 112 ALSRRDEPPQGPTLRIAAHLTGSSKRSSASPHNYLSYRGIGHKHSWESSRRGHSFLYNV 171  
 Qy 200 TFSNGKLIVNQDGFYYLYANICFRHHET----SG--DLATEYLQLMVYVTKTSIKIPSSH 253  
 | : | : | | | | : | | | : | | : | | : | : | :  
 Db 172 ELWNGELVVPQTGFYYIYSQTYFRFRENEDSDGLLERIKNPKQLVQYIYKLT-NYPDPI 230  
 Qy 254 TLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSSLDPDQDATYFGAFKV 313  
 | | | | | | : | : | | | : | : | : | : | : | : | : | : | :  
 Db 231 LLMKSARTSCWSKKAHEYGLYSVYQGGVFQLKREDRIFVSVSNSDIVDMDKEASFFGAFMI 290

# RESULT 3

Q9DDZ5

ID Q9DDZ5 PRELIMINARY; PRT; 214 AA.

AC Q9DDZ5;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE TRAIL-like protein.

GN TNFSF10L.

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI\_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Bobe J., Goetz F.W.;  
RT "Molecular cloning and expression of a TNF receptor and two TNF  
RT ligands in the fish ovary."  
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).  
DR EMBL; AF250041; AAG47640.1; -.  
DR HSSP; P50591; 1D2Q.  
DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR006052; TNF\_family.  
DR InterPro; IPR008983; TNF\_like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
SQ SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Qy	118	RIKQAFQGA	VQKELQHIVGSQH	IRAEKAMVDG	SWL	DLAK-RSKLEAQ	PF	AHLT	TINATDIP	176	
Db	2	KLAEGIKAY	ISKV	TD	SIISKQ	TLHAARTQ	THSYNTT	GS	KFMTTVMQ	RPSAHLTLSSASDN	61
Qy	177	S-----	GSHK	VSLSSWYH	DRGWAKI	SNMTFS	NGKLIV	NQDGF	YYLYANICF	222	
Db	62	SRPQSD	MHQ	PQ	FDLHQ	SCRHPVHT	WANKS	FGAHL	YNMTLT	NGRLRVPQDGRYYLYSQVYF	121
Qy	223	RHHETS-GD	LATEYLQ	LMVYV-TK	TSIKIPSS	SHTLMKGG	STKYW	SGNSEF	HFYSIN	VGGF	280
Db	122	RYPSPSD	SDSQSSV	SHQLVQ	CIYKKT	SYLNPIQ--	LLKGVG	TKC	WAPDAEY	ALHSVYQGGL	179
Qy	281	FKLRSGEE	ISIEVSN	PSLLDP	DQDATY	FGAFKV	313				
Db	180	FELRAGDE	VFVSVSS	PTM	VYGED	SSSYF	GAFRL	212			

RT ovary.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY057941; AAL23702.1; -.  
 DR HSSP; O35235; 1IQA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;

Query Match 12.8%; Score 216.5; DB 13; Length 287;  
 Best Local Similarity 24.7%; Pred. No. 3.5e-11;  
 Matches 61; Conservative 57; Mismatches 104; Indels 25; Gaps 6;

Qy 80 SEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAQVQKELQHIVGSQH 139  
 | : | : | : | : : : : : | : : : :  
 Db 51 SSEELRCLQLINQQQEGSNLEEL-----ISNQSCLKLANTIKAYVATVTENVISRSV 102  
  
 Qy 140 I-RAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIP-----SGSHKVSLSW 187  
 : | : : : | : | : | : : : : : | : : : :  
 Db 103 VNEAQKSYFNISEGQVA--TKTLGKPSAHLIFRPQNPQDQSSRRFNGLSQSCRHAITRW 160  
  
 Qy 188 YHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMVYVT-KTS 246  
 : : | : : : | : | : | : : : : | : : : :  
 Db 161 EDSTIHSHLQNITYRDGRLRVNQAGKYVYSQIYFRYSRDGAGARVSVPLVQCINWKTS 220  
  
 Qy 247 IKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEISIEVSNPSLLDPDQDAT 306  
 | : | : | : | : : : : | : | : : : : : | : : : :  
 Db 221 YSQPI--LLLKGVGTCWAPEAEYGLHALYQGGLFELKAGDELFSVSVSSLAIDYSDAAS 278  
  
 Qy 307 YFGAFKV 313  
 ||||| : :  
 Db 279 YFGAFRL 285

# RESULT 5

Q8K3G0

ID Q8K3G0 PRELIMINARY; PRT; 287 AA.  
 AC Q8K3G0;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TNF-related apoptosis inducing ligand.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=DA;  
 RA Mueller A.M., Giegerich G.;  
 RT "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY115578; AAM49797.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 12.8%; Score 215.5; DB 11; Length 287;  
 Best Local Similarity 24.2%; Pred. No. 4.3e-11;  
 Matches 73; Conservative 59; Mismatches 113; Indels 57; Gaps 14;

Qy 42 PAASRSMFVALLGLGLQVV---CSVAL-FFYFRAQMD--PNRISEDGTHCIYRILRLHE 95  
 |: |: : :: : | ||: :||: : || :: : |: | | : |  
 Db 10 PSFSQHFTMTVICIVLLQVLLQALTVAVTYMYFNNEVKQLQDNYSKIGLACFSK-----E 64  
 Qy 96 NADFQDTTLESQDTKLIPDSCRRKQAFQGAQVQKELQHIVGSQHIRA-EKAMVDGSWLDL 154  
 : || |:| | :: | ::| ::| :: :| || :  
 Db 65 DGDFWDST----DEGILNRPCLVK-----RQLYQLIEEVTLRTEFT-----IST 106  
 Qy 155 AKRSKLEAQPF-----AHLT-----INATDIPSGSHKVSL----SSWYHD-RGWA 194  
 :| | ||:| | || :| :| || :  
 Db 107 VPEKQLSTPPLPRGRRPQRVAAHITGITRRSNLALIPISKDGKTLGQKIETWESSRRGHS 166  
 Qy 195 KISNMTFSNGKLIVNQDGFYLYLANICFRHHETSGDLAT-----EYLQLMVYVTKTSIK 248  
 :::: ||:|:: ::| ||:|: :| | | | :| :| :  
 Db 167 FLNHVHLRNGELVIQEGLYYIYSQTYFRFEAKEASKTVSKDGGRIKQMVQYIYKYT-S 225  
 Qy 249 IPSSHTLMKGGSTKYWSGNSEFHFYSINVGFFKLRSGEEISIEVSNPSLLDPDQDATYF 308  
 | ||| || :|: ||| || |:|: :| :|:| |:| | :|:|  
 Db 226 YPDPIILLMKSARNSCWSREAEYGLYSIQGGLFELKENDRIFVSVTNEHLMDLDHEASFF 285  
 Qy 309 GA 310  
 ||  
 Db 286 GA 287

# RESULT 6

Q861W5

ID Q861W5 PRELIMINARY; PRT; 280 AA.  
 AC Q861W5;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Fas ligand.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99053606; PubMed=9839871;  
 RA Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Tsubota K.,  
 RA Mikami T., Ohno K., Watari T., Tsujimoto H., Hasegawa A.;  
 RT "Molecular cloning of feline Fas antigen and Fas ligand cDNAs."  
 RL Vet. Immunol. Immunopathol. 65:161-172(1998).  
 DR EMBL; AB009280; BAC76426.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 280 AA; 31361 MW; 6AA7E2DE1F1A6B5C CRC64;

Query Match 11.5%; Score 194.5; DB 6; Length 280;  
 Best Local Similarity 22.8%; Pred. No. 3.3e-09;  
 Matches 74; Conservative 40; Mismatches 98; Indels 113; Gaps 12;

Qy 20 GGPG----APHEGPLHAPPPAPHPQPPAASRSM-----FVALLGLG 56  
 | | | | | | | | | | | | : | | | | |  
 Db 38 GRPGQRRPPPPPPPTLPPPPPPPLPPLPLPPLKTRRDHNTGLCLLVMMFFMVLVALVGLG 97  
 Qy 57 LGQVVCVSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSC 116  
 | | : | | | | | | | : : : | :  
 Db 98 LG-----MFQLFHLQ-----KELAELESTSQKH----- 121  
 Qy 117 RRIKQAFQGA VQKELQHIVGSQH IRAEKAMVDG SWLDLAKRSKLEAQPF AHLT--INATD 174  
 | | : : | : : | | | : | | | | :  
 Db 122 -----VASSLEKQIGQLNPPSEKR-----ELRKVAHLTGKPNRS 156  
 Qy 175 IPSGSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATE 234  
 | | | | | : | : : | | : | | : : | : :  
 Db 157 IP-----LEWEDTYGIALVSGVKYKKGGLVINDTGMYFVYSKVNFRGQSCN----NQ 204  
 Qy 235 YLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKLRS GEE 288  
 | | | : | | | : | | : : | : : | | :  
 Db 205 PLNHKVMYRNS--KYPQDLVLMEGKMMNYCTTGQMWARSS-----YLGA VFNLT SADH 255  
 Qy 289 ISIEVSNPSLLDPDQDATYFGAFKV 313  
 : : | | | : : | : | : :  
 Db 256 LYVNVSELSLVSFEEKSTFFGLYKL 280

RESULT 7

Q7TMV9

ID Q7TMV9 PRELIMINARY; PRT; 279 AA.  
 AC Q7TMV9;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tnfsf6 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
 RA Strausberg R.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC052866; AAH52866.1; -.  
 SQ SEQUENCE 279 AA; 31416 MW; C2972E2728FBBB7B CRC64;

Query Match 11.1%; Score 187.5; DB 11; Length 279;  
 Best Local Similarity 21.7%; Pred. No. 1.4e-08;  
 Matches 70; Conservative 46; Mismatches 105; Indels 101; Gaps 11;

Qy 13 RGSEEMGGGPGAPHEGPLHAPPPAPHQP-----PAASRSMFVALLGLGL 57  
 || :: | | || | | | | | : |||:|:|  
 Db 38 RGPDQRRPPPPPPVSPPLPPSQPLPLPLTPLKKKDHTNLWLPLPVVFFMVLVALVGMGL 97  
 Qy 58 GQVVCVALFFYFRAQMDPNRISEDGTHCIYRIIRLHENADFQDTTLESQDTKLIPDSCR 117  
 | :|:| |  
 Db 98 G-----MYQLFHL----- 105



Qy 118 RIKQAFQGAVQKELQHI--VGSQHRA---EKAMVDGSWLDLAKRSKLEAQPFahlTINA 172  
 |||| : :| :: || : : | | : |||| |  
 Db 106 -----QKELAELeFTNQSLKVSSFEKQIANPS----TPSEKKEPRSVaHLtGN- 150  
 Qy 173 TDIPSGSHKVSLS-SWYHdRGWAKISNMtFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231  
 | | : | | | | : : | | : : | | : : | : :  
 Db 151 -----PHSRsIPLEWEDTYGTALISGVKYKKGGLVINETGLYfVYsKVYFRGQSCN--- 201  
 Qy 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEfHFYSINVGgFFKLRSgEEISi 291  
 : | || : | | || : | : : | : : | | | : : :  
 Db 202 -NQPLNHKVYMRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSHLGAVfNLtSADHLYV 257  
 Qy 292 EVSNPSLLDPDQDATYFGAFKV 313  
 : | || : : | : || : :  
 Db 258 NISQLSLINFEESKtFFGLYKL 279

RESULT 8

Q8K3Y8

ID Q8K3Y8 PRELIMINARY; PRT; 252 AA.  
 AC Q8K3Y8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TNF superfamily ligand TL1A.  
 GN TNFSF15.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=21909416; PubMed=11911831;  
 RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,  
 RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,  
 RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,  
 RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;  
 RT "TL1A is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T  
 RT cell costimulator.";  
 RL Immunity 16:479-492(2002).  
 DR EMBL; AF520786; AAM77367.1; -.  
 DR MGD; MGI:2180140; Tnfsf15.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 252 AA; 27723 MW; BB901C9350119E0F CRC64;

Query Match 10.9%; Score 184.5; DB 11; Length 252;  
 Best Local Similarity 26.2%; Pred. No. 2.3e-08;  
 Matches 64; Conservative 39; Mismatches 100; Indels 41; Gaps 10;

```

Qy      105 ESQDTKLIPDSCRRIKQAFQGAVQK-----ELQHIVG-SQHIRAEKAMVDGSW 151
      |   ::||: ||   :| |   :   : | | : | : | |
Db      11 EGVPEVVLPEGCRHRPEARAGLAARSKACLALTCCLLSFPILAGLSTLLMAGQLRVP GK- 69

Qy      152 LDLAKRSKLE-----AQPF AHLTI-NATDIPSGSHKVSLSWYHDRGWAK 195
      | | : |   : | |||| | | : : | | | | |
Db      70 -DCMLRAITEERSESPSQQVYSPPRGK PRAHLTIKKQTPAPHLKNQLSALHWEHDLGMAF 128

Qy      196 ISN-MTFSNGKLIVNQDGFYYLYANICFR-HHETSGDLA-----TEYLQLMVYVTKTSIK 248
      | | : | | : : | | : : | | | | : : : | : | :
Db      129 TKNGMKYINKSLVIPESGDYFIYSQITFRGTTSVCGDISRGRPNKPD SITVVITKVADS 188

Qy      249 IPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD-PDQDATY 307
      |   | : | :   | : | | : : | | | | : : : || : | :
Db      189 YPEPARLLTGSKSVCEISNN--WFQSLYLGAMFSLEEGDRLMVNVSDISLVDYTKEDKTF 246

Qy      308 FGAF 311
      ||||
Db      247 FGAF 250
  
```

# RESULT 9

Q80YZ0

```

ID   Q80YZ0          PRELIMINARY;          PRT;    252 AA.
AC   Q80YZ0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   BM20K13.3 (Tumor necrosis factor (Ligand) superfamily, member
DE   15).
GN   TNFSF15.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sycamore N.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL691468; CAD83021.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR008983; TNF_like.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS50049; TNF_2; 1.
  
```

SQ SEQUENCE 252 AA; 27725 MW; A63ABDCC9E969E0F CRC64;

Query Match 10.7%; Score 179.5; DB 11; Length 252;  
Best Local Similarity 25.8%; Pred. No. 6.5e-08;  
Matches 63; Conservative 40; Mismatches 100; Indels 41; Gaps 10;

```
Qy      105 ESQDTKLIPDSCRRIKQAFQGAVQK-----ELQHIVG-SQHIRAEKAMVDGSW 151
      |   ::||: ||   :| |   :   : | | : | : | |
Db      11 EGVPEVVLPEGCRHRPEARAGLAARSKACLALTCCLLSFPILAGLSTLLMAGQLRVPGK- 69

Qy      152 LDLAKRSKLE-----AQPF AHLTI-NATDIPSGSHKVSLSWYHDRGWAK 195
      |   | : |   : | |||| | |   ::| | || | |
Db      70 -DCMLRAITEERSESPSQQVYSPPRGKPAHLTIKKQTPAPHLKNQLSALHWEHDLGMAF 128

Qy      196 ISN-MTFSNGKLIVNQDGFYLYLANICFR-HHETSGDLA-----TEYLQLMVYVTKTSIK 248
      | | : | |:: : | |::: | ||   ||::   :   : : || :
Db      129 TKNMGKYINKSLVIPESGDYFIYSQITFRGTTSVCGDISRGRPNKPDSITMVITKVADS 188

Qy      249 IPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRS GEEISIEVSNPSLLD-PDQDATY 307
      |   | : | :   | : | | : : | | | : : : || : || :
Db      189 YPEPARLLTGSKSVCEISNN--WFQSLYLGATFSLEEGDRLMVNVSDISLVDYTKEDKTF 246

Qy      308 FGAF 311
      ||||
Db      247 FGAF 250
```

RESULT 10

Q8K3Y7

```
ID   Q8K3Y7          PRELIMINARY;          PRT;    252 AA.
AC   Q8K3Y7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   TNF superfamily ligand TL1A.
GN   TNFSF15.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=21909416; PubMed=11911831;
RA   Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA   Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA   Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA   Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT   "TL1A is a TNF-like ligand for DR3 and TR6/DcR3 and functions as a T
RT   cell costimulator.";
RL   Immunity 16:479-492(2002).
DR   EMBL; AF520787; AAM77368.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR006052; TNF_family.
```





DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 215 215  
 SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;

Query Match 8.3%; Score 139.5; DB 11; Length 215;  
 Best Local Similarity 26.5%; Pred. No. 0.00021;  
 Matches 40; Conservative 27; Mismatches 51; Indels 33; Gaps 5;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221  
 :| ||: | |: | | | :| | :|:| || |: :  
 Db 79 KPAHVAVANQTE-----EQIQWLSRRANALLANGMELIDNQLVVPADGLYLIYSQVL 130  
  
 Qy 222 FRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNSE 269  
 |: | : |: | |: :| | :| | | |  
 Db 131 FK-----GQGCSSYVLLTHTVSRFAVSQYQDKVNLLSAIKSPCPKESLEGAEFKPW----- 180  
  
 Qy 270 FHFYSINVGGFKKLRSGEEISIEVSNPSLLD 300  
 : | :| |: |: |: | | :| | |  
 Db 181 --YEPIYLGGVFELQKGDRLSAEVNLP SYLD 209

# RESULT 13

Q91ZL4

ID Q91ZL4 PRELIMINARY; PRT; 156 AA.  
 AC Q91ZL4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor alpha (Fragment).  
 OS Sigmodon hispidus (Hispid cotton rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Sigmodon.  
 OX NCBI\_TaxID=42415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Blanco J.C., Pletneva L.M., Prince G.A.;  
 RT "Sigmodon hispidus cytokines, chemokines and interferons."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF421388; AAL18818.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.

DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 156 AA; 17303 MW; DC565F3BC3C826E4 CRC64;

Query Match 8.2%; Score 137.5; DB 11; Length 156;  
 Best Local Similarity 27.0%; Pred. No. 0.0002;  
 Matches 43; Conservative 25; Mismatches 68; Indels 23; Gaps 7;

Qy 160 LEAQPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYA 218  
 | :| ||: | | | :| | | :|:: || | :|:  
 Db 8 LSDKPVAVHVAN-----QQAEEQLEWLSQRANALLANGMDLRNNQLVIPADGLYLVYS 60  
 Qy 219 NICFRHHETSG-DLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFH 271  
 : |: | :| | : : | | :|| | :| | |  
 Db 61 QVLFKGLGRSNCELLTHTVSRIAVSYEDKVNLLSAIKSPCPKETPQGAE LKPW----- 113  
 Qy 272 FYSINVGGFFKLRSGEIEISIEVSNPSLLD-PDQDATYFG 309  
 : | :|| |:| |: :| ||::| || : |||  
 Db 114 YEPIYLGGVFQLEKGDRLSAEVNHPKYLDFAESGQVYFG 152

# RESULT 14

## Q80XA4

ID Q80XA4 PRELIMINARY; PRT; 232 AA.  
 AC Q80XA4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor precursor (Fragment).  
 GN TNF.  
 OS Peromyscus maniculatus (Deer mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Peromyscus.  
 OX NCBI\_TaxID=10042;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Green R.M., Herbst M.M., Schountz T.;  
 RT "Cloning of the deer mouse tumor necrosis factor gene."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY249143; AAP03078.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Signal.  
 FT SIGNAL 1 20 Potential.  
 FT CHAIN 80 >232 tumor necrosis factor.  
 FT NON\_TER 232 232  
 SQ SEQUENCE 232 AA; 25704 MW; E48A9379DB4F216D CRC64;

Query Match 8.2%; Score 137.5; DB 11; Length 232;  
 Best Local Similarity 25.9%; Pred. No. 0.00036;  
 Matches 42; Conservative 27; Mismatches 58; Indels 35; Gaps 7;

Qy 163 QPFAHLTINATDIPSGSHKVSLS-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220  
 :| ||: | |:| | | :|| | :||: || |: :  
 Db 90 KPAHVVAN-----HQVDEQLEWLSRRANALLANGMDLKDNLVIPADGLYLIVYSQV 141  
 Qy 221 CFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYWSGNS 268  
 |: | :|: | |: :|| | :| | |  
 Db 142 LFK-----GQGCSNYVLLTHTVSRFAVSIEDKVNLLSAIKSPCPKETPEGSELKPW---- 192  
 Qy 269 EFHFYSINVGFFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309  
 : | :|| |:| |: :| ||: | || : |||  
 Db 193 ---YEPIYLGGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFG 231

# RESULT 15

097543

ID 097543 PRELIMINARY; PRT; 149 AA.  
 AC 097543;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Tumor necrosis factor alpha (Fragment).  
 GN TNF-ALPHA.  
 OS Aotus nancymaae (Ma's night monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
 OX NCBI\_TaxID=37293;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;  
 RT "Identification, cloning and sequencing of different interleukin genes  
 RT in 4 Aotus species."  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF014513; AAD01539.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.



DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 149 149  
 SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match 7.9%; Score 133; DB 6; Length 149;  
 Best Local Similarity 25.5%; Pred. No. 0.00048;  
 Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

Qy 163 QPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221  
 :| ||: | : : | : | :| : : :| :| :| : :  
 Db 4 KPAHVAVAN----PQAEGQL---QWLNRRANALLANGVELRDNQIVVPSEGLYLIYSQVL 56  
 Qy 222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273  
 | : :| | : : | || :|| | :| | | :  
 Db 57 FKGQGCPSHVLTLTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YE 109  
 Qy 274 SINVGGFFLRSGEIEVSNPILLD-PDQDATYFG 309  
 | :|| | :| : :| | :| | : |||  
 Db 110 PIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFG 146

Search completed: February 25, 2004, 16:30:28  
 Job time : 52 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 25, 2004, 16:13:36 ; Search time 17 Seconds  
(without alignments)  
970.955 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	1685	100.0	317	1	TN11_HUMAN	014788	h tumor nec
2	1417.5	84.1	316	1	TN11_MOUSE	035235	m tumor nec
3	1396.5	82.9	318	1	TN11_RAT	Q9ese2	r tumor nec
4	251.5	14.9	281	1	TN10_HUMAN	P50591	homo sapien
5	248	14.7	291	1	TN10_MOUSE	P50592	mus musculu
6	200	11.9	282	1	TNF6_PIG	Q9bea8	sus scrofa
7	189	11.2	281	1	TNF6_HUMAN	P48023	homo sapien
8	186	11.0	280	1	TNF6_MACMU	Q9myl6	macaca mula
9	184.5	10.9	279	1	TNF6_MOUSE	P41047	mus musculu
10	182.5	10.8	280	1	TNF6_CERTO	Q9bdn1	cercocobus
11	176.5	10.5	261	1	TNF5_BOVIN	P51749	bos taurus
12	175.5	10.4	278	1	TNF6_RAT	P36940	rattus norv
13	169.5	10.1	261	1	TNF5_CALJA	Q9bdn3	callithrix
14	167.5	9.9	261	1	TNF5_AOTTR	Q9bdm3	aotus trivi
15	158.5	9.4	261	1	TNF5_HUMAN	P29965	homo sapien
16	155.5	9.2	261	1	TNF5_MACMU	Q9bdc7	macaca mula
17	155	9.2	272	1	TNF5_CHICK	Q9i8d8	gallus gall

18	152.5	9.1	261	1	TNF5_PIG	Q95mq5	sus scrofa
19	152	9.0	260	1	TNF5_FELCA	O97605	felis silve
20	146	8.7	234	1	TNFA_CAVPO	P51435	cavia porce
21	145.5	8.6	239	1	TN14_MOUSE	Q9qyh9	mus musculu
22	145	8.6	174	1	TN15_HUMAN	O95150	homo sapien
23	145	8.6	260	1	TNF5_CANFA	O97626	canis famil
24	143	8.5	240	1	TNF5_MACNE	Q9bdm7	macaca neme
25	141.5	8.4	235	1	TNFA_MOUSE	P06804	mus musculu
26	140.5	8.3	235	1	TNFA_RABIT	P04924	oryctolagus
27	139	8.2	233	1	TNFA_SAISC	Q8mkg8	saimiri sci
28	137	8.1	234	1	TNFA_SHEEP	P23383	ovis aries
29	136	8.1	234	1	TNFA_CAPHI	P13296	capra hircu
30	134.5	8.0	310	1	TNFC_MARMO	Q9jml0	marmota mon
31	134	8.0	233	1	TNFA_MACFA	P79337	macaca fasc
32	134	8.0	240	1	TN14_HUMAN	O43557	homo sapien
33	133	7.9	232	1	TNFA_PANTR	Q8hzd9	pan troglod
34	133	7.9	233	1	TNFA_CANFA	P51742	canis famil
35	133	7.9	233	1	TNFA_HUMAN	P01375	homo sapien
36	133	7.9	233	1	TNFA_MACMU	P48094	macaca mula
37	132.5	7.9	235	1	TNFA_PERLE	P36939	peromyscus
38	131.5	7.8	235	1	TNFA_RAT	P16599	rattus norv
39	130.5	7.7	306	1	TNFC_MOUSE	P41155	mus musculu
40	130	7.7	233	1	TNFA_PAPSP	P33620	papio sp. (
41	129.5	7.7	233	1	TNFA_MARMO	O35734	marmota mon
42	129	7.7	233	1	TNFA_PAPAN	P59695	papio anubi
43	129	7.7	233	1	TNFA_PAPHU	O77510	papio hamad
44	128	7.6	234	1	TNFA_HORSE	P29553	equus cabal
45	126.5	7.5	233	1	TNFA_BOVIN	Q06599	bos taurus

#### ALIGNMENTS

##### RESULT 1

##### TN11\_HUMAN

ID TN11\_HUMAN STANDARD; PRT; 317 AA.  
AC O14788; O14723; Q96Q17; Q9P2Q3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
DE differentiation factor) (ODF).  
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Bone marrow, and Peripheral blood;  
RX MEDLINE=98032977; PubMed=9367155;  
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
RA Galibert L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth

RT and dendritic-cell function."  
 RL Nature 390:175-179(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Lymph node;  
 RX MEDLINE=98227661; PubMed=9568710;  
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
 RA Boyle W.J.;  
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
 RT differentiation and activation."  
 RL Cell 93:165-176(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RA Ikeda T., Kuroyama H., Hirokawa K.;  
 RT "Determination of human RANKL isoforms."  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE OF 73-317 FROM N.A.  
 RC TISSUE=Thymocytes;  
 RX MEDLINE=97460112; PubMed=9312132;  
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,  
 RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,  
 RA Choi Y.;  
 RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells."  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Tongue;  
 RX MEDLINE=20175237; PubMed=10708588;  
 RA Nagai M., Kyakumoto S., Sato N.;  
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA  
 RT encoding a secreted form of ODF/TRANCE that induces osteoclast  
 RT formation."  
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);  
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by  
 CC proteolytic processing (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O14788-1; Sequence=Displayed;  
 CC Name=2; Synonyms=SODF;  
 CC IsoId=O14788-2; Sequence=VSP\_006447;  
 CC Name=3;

```

CC      IsoId=O14788-3; Sequence=VSP_006446;
CC      -!- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK
CC          IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC          PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC      -!- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
CC      -!- PTM: The soluble form of isoform 1 derives from the membrane form
CC          by proteolytic processing (By similarity). The cleavage may be
CC          catalyzed by ADAM17.
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF019047; AAB86811.1; -.
DR      EMBL; AF053712; AAC39731.1; -.
DR      EMBL; AB064269; BAB79694.1; -.
DR      EMBL; AB061227; BAB71768.1; -.
DR      EMBL; AB064270; BAB79695.1; -.
DR      EMBL; AF013171; AAC51762.1; -.
DR      EMBL; AB037599; BAA90488.1; -.
DR      HSSP; P50591; 1DOG.
DR      Genew; HGNC:11926; TNFSF11.
DR      MIM; 602642; -.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0005887; C:integral to plasma membrane; NAS.
DR      GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      GO; GO:0030316; P:osteoclast differentiation; NAS.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR008983; TNF_like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; FALSE_NEG.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW      Signal-anchor; Alternative splicing.
FT      CHAIN          1      317      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 11, MEMBRANE FORM.
FT      CHAIN          140     317      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 11, SOLUBLE FORM (BY SIMILARITY).
FT      DOMAIN          1      47      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM        48      68      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                     (POTENTIAL).
FT      DOMAIN          69     317      EXTRACELLULAR (POTENTIAL).
FT      SITE            139     140     CLEAVAGE (BY SIMILARITY).
FT      CARBOHYD        171     171     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        198     198     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      VARSPLIC         1      47      Missing (in isoform 3).
FT                                     /FTId=VSP_006446.
FT      VARSPLIC         1      73      Missing (in isoform 2).

```

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FT                               /FTId=VSP_006447.
FT  CONFLICT      194      194      A -> G (IN REF. 4).
SQ  SEQUENCE      317 AA;  35478 MW;  766176446348097F CRC64;

  Query Match      100.0%;  Score 1685;  DB 1;  Length 317;
  Best Local Similarity 100.0%;  Pred. No. 3.6e-138;
  Matches 317;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPAPHPQPPAASRSMFVALLGLGLGQV 60

Qy     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAPHLTINATDIPSGSH 180

Qy    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMV 240

Qy    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEESISIEVSNPSLLD 300

Qy    301 PDQDATYFGAFKVRDID 317
      ||||||||||||||||
Db    301 PDQDATYFGAFKVRDID 317

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# RESULT 2

## TN11\_MOUSE

```

ID  TN11_MOUSE      STANDARD;      PRT;      316 AA.
AC  O35235; O35306; Q9JJK8; Q9JJK9; Q9R1Y0;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Tumor necrosis factor ligand superfamily member 11 (Receptor activator
DE  of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-
DE  induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
DE  differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)
DE  (OCIF).
GN  TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RC  TISSUE=Hybridoma;
RX  MEDLINE=97460112; PubMed=9312132;
RA  Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA  Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA  Choi Y.;

```

RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family  
 RT that activates c-Jun N-terminal kinase in T cells.";  
 RL J. Biol. Chem. 272:25190-25194(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Thymic lymphoma;  
 RX MEDLINE=98032977; PubMed=9367155;  
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
 RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,  
 RA Galibert L.;  
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=98227661; PubMed=9568710;  
 RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,  
 RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,  
 RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,  
 RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,  
 RA Boyle W.J.;  
 RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast  
 RT differentiation and activation.";  
 RL Cell 93:165-176(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow stroma;  
 RX MEDLINE=98188248; PubMed=9520411;  
 RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,  
 RA Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,  
 RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;  
 RT "Osteoclast differentiation factor is a ligand for  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical  
 RT to TRANCE/RANKL.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=129;  
 RX MEDLINE=99214075; PubMed=10196481;  
 RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,  
 RA Ueda M., Higashio K.;  
 RT "Cloning and characterization of the gene encoding mouse osteoclast  
 RT differentiation factor.";  
 RL Gene 230:121-127(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=21150053; PubMed=11250921;  
 RA Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;  
 RT "Determination of three isoforms of the receptor activator of nuclear  
 RT factor-kappaB ligand and their differential expression in bone and  
 RT thymus.";  
 RL Endocrinology 142:1419-1426(2001).  
 RN [7]  
 RP SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION.  
 RX MEDLINE=99240759; PubMed=10224132;  
 RA Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H.,

RA Schloendorff J., Tempst P., Choi Y., Blobel C.P.;  
 RT "Evidence for a role of a tumor necrosis factor-alpha  
 RT (TNF-alpha)-converting enzyme-like protease in shedding of TRANCE, a  
 RT TNF family member involved in osteoclastogenesis and dendritic cell  
 RT survival.";  
 RL J. Biol. Chem. 274:13613-13618(1999).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316.  
 RX MEDLINE=21464816; PubMed=11581298;  
 RA Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.;  
 RT "Crystal structure of the TRANCE/RANKL cytokine reveals determinants  
 RT of receptor-ligand specificity.";  
 RL J. Clin. Invest. 108:971-979(2001).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.  
 RX MEDLINE=21839021; PubMed=11733492;  
 RA Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T.;  
 RT "Crystal structure of the extracellular domain of mouse RANK ligand at  
 RT 2.2-A resolution.";  
 RL J. Biol. Chem. 277:6631-6636(2002).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted  
 CC (isoforms 1 and 2); Cytoplasmic (isoform 3).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;  
 CC IsoId=O35235-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=O35235-2; Sequence=VSP\_006449;  
 CC Name=3;  
 CC IsoId=O35235-3; Sequence=VSP\_006448;  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT  
 CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS  
 CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE  
 CC TRABECULAR BONE AND LUNG.  
 CC -!- PTM: N-glycosylated.  
 CC -!- PTM: The soluble form of isoform 1 derives from the membrane form  
 CC by proteolytic processing. The cleavage may be catalyzed by  
 CC ADAM17. A further shorter soluble form was observed.  
 CC -!- DISEASE: Deficiency in TNFSF11 results in failure to form lobulo-  
 CC alveolar mammary structures during pregnancy, resulting in death  
 CC of newborns. Trance-deficient mice show severe osteopetrosis, with  
 CC no osteoclasts, marrow spaces, or tooth eruption, and exhibit  
 CC profound growth retardation at several skeletal sites, including  
 CC the limbs, skull, and vertebrae and have marked chondrodysplasia,  
 CC with thick, irregular growth plates and a relative increase in  
 CC hypertrophic chondrocytes.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----



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 CC -----

DR EMBL; AF013170; AAC71061.1; -.  
 DR EMBL; AF019048; AAB86812.1; -.  
 DR EMBL; AF053713; AAC40113.1; -.  
 DR EMBL; AB008426; BAA25425.1; -.  
 DR EMBL; AB022039; BAA36970.1; -.  
 DR EMBL; AB022036; BAA36970.1; JOINED.  
 DR EMBL; AB022037; BAA36970.1; JOINED.  
 DR EMBL; AB022038; BAA36970.1; JOINED.  
 DR EMBL; AB032771; BAA97257.1; -.  
 DR EMBL; AB032772; BAA97258.1; -.  
 DR EMBL; AB036798; BAA97259.1; -.  
 DR PDB; 1JTZ; 28-JAN-03.  
 DR PDB; 1IQA; 14-JAN-03.  
 DR MGD; MGI;1100089; Tnfsf11.  
 DR GO; GO:0009887; P:organogenesis; IMP.  
 DR GO; GO:0001503; P:ossification; IMP.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 DR PROSITE; PS0049; TNF\_2; 1.  
 KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;  
 KW Signal-anchor; 3D-structure; Alternative splicing.  
 FT CHAIN 1 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 11, MEMBRANE FORM.  
 FT CHAIN 139 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 11, SOLUBLE FORM.  
 FT DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).  
 FT SITE 138 139 CLEAVAGE.  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 117 Missing (in isoform 3).  
 FT /FTid=VSP\_006448.  
 FT VARSPLIC 14 44 SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (in  
 FT isoform 2).  
 FT /FTid=VSP\_006449.  
 FT CONFLICT 99 99 G -> D (IN REF. 2).  
 FT CONFLICT 141 143 MISSING (IN REF. 5).  
 FT STRAND 164 169  
 FT TURN 171 172  
 FT STRAND 181 182  
 FT STRAND 186 187  
 FT TURN 191 192

Query Match 84.1%; Score 1417.5; DB 1; Length 316;  
Best Local Similarity 84.3%; Pred. No. 4.7e-115;  
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

### RESULT 3

TN11 RAT

ID TN11 RAT STANDARD; PRT; 318 AA.

AC 09ESE2; 091ZI9;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator  
DE of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-  
DE induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast  
DE differentiation factor) (ODF).

GN TNFSF11 OR RANKL OR TRANCE OR OPGL.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

```
RC TISSUE=Tibial bone;
```

RX MEDLINE=20540945; PubMed=11092398;

RA Xu J.K., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,  
 RA Zheng M.H.;  
 RT "Cloning, sequence and functional characterization of the rat  
 RT homologue of receptor activator of NF-kB ligand.";  
 RL J. Bone Miner. Res. 15:2178-2186(2000).  
 RN [2]  
 RP SEQUENCE OF 266-318 FROM N.A.  
 RC STRAIN=Fischer 344;  
 RX MEDLINE=21662371; PubMed=11804028;  
 RA Odgren P.R., Kim N., van Wesenbeeck L., MacKay C., Mason-Savas A.,  
 RA Safadi F.F., Popoff S.N., Lengner C., van-Hul W., Choi Y.,  
 RA Marks S.C. Jr.;  
 RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in  
 RT the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";  
 RL Int. J. Dev. Biol. 45:853-859(2001).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to  
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.  
 CC Augments the ability of dendritic cells to stimulate naive T-cell  
 CC proliferation. May be an important regulator of interactions  
 CC between T cells and dendritic cells and may play a role in the  
 CC regulation of the T cell-dependent immune response. May also play  
 CC an important role in enhanced bone-resorption in humoral  
 CC hypercalcemia of malignancy.  
 CC -!- SUBUNIT: Homotrimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 DR EMBL; AF187319; AAG17031.1; -.  
 DR EMBL; AF425669; AAL23963.1; -.  
 DR HSSP; P50591; 1D0G.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;  
 KW Signal-anchor.  
 FT CHAIN 1 318 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 11, MEMBRANE FORM.  
 FT CHAIN 141 318 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 11, SOLUBLE FORM.  
 FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 69 318 EXTRACELLULAR (POTENTIAL).  
 FT SITE 140 141 CLEAVAGE (BY SIMILARITY).  
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 317 317 I -> M (IN REF. 2).  
 SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

Query Match 82.9%; Score 1396.5; DB 1; Length 318;  
 Best Local Similarity 82.4%; Pred. No. 3.1e-113;  
 Matches 262; Conservative 19; Mismatches 36; Indels 1; Gaps 1;

QY 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPAPHPQPPAASRSMFVALLGLGLGQ 59  
 ||||:|||| ||||| || ||||| || ||| ||||| ||:|||||||  
 Db 1 MRRANRDYGYKLYRGSEEMGSCPGVPHEGPLHPAPSAPAPAPPPAASRFMFLALLGLGLGQ 60  
 QY 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119  
 ||||:|||| ||||| ||||| || ||||| || ||:||||: ||: |||||:  
 Db 61 VVCSIALFLYFRAQMDPNRISEDSTRCFYRILRLRENTGLQDSTLESEDTEALPDSCRMM 120  
 QY 120 KQAFQGA VQKELQHIVGSQH IRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179  
 ||||| ||||:||||| || ||||:||||: || ||||| |||||  
 Db 121 KQAFQGA VQRELQHIVGPQRFSGVPAMMEGSWLDVARRGKPEAQPFAHLTINAADIPSGS 180  
 QY 180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQIM 239  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||  
 Db 181 HKVSLSSWYHDRGWAKISNMTLSNGKLIVNQDGFYLYANICFRHHETSGSVPADYLQIM 240  
 QY 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISIEVSNPSLL 299  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||: |||||  
 Db 241 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVG GFFKL RAGEEISVQVSNPSLL 300  
 QY 300 DPDQDATYFGAFKVRDID 317  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 301 DPDQDATYFGAFKVQDID 318

#### RESULT 4

##### TN10\_HUMAN

ID TN10\_HUMAN STANDARD; PRT; 281 AA.  
 AC P50591;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related  
 DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).  
 GN TNFSF10 OR TRAIL OR APO2L.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96111955; PubMed=8777713;  
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,  
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,

RA Goodwin R.G.;  
 RT "Identification and characterization of a new member of the TNF  
 RT family that induces apoptosis.";  
 RL Immunity 3:673-682(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=96278649; PubMed=8663110;  
 RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,  
 RA Ashkenazi A.;  
 RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor  
 RT necrosis factor cytokine family.";  
 RL J. Biol. Chem. 271:12687-12690(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.  
 RX MEDLINE=20017054; PubMed=10549288;  
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,  
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
 RT complex with death receptor 5.";  
 RL Mol. Cell 4:563-571(1999).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.  
 RX PubMed=10542098;  
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Screaton G.R.;  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.  
 RX MEDLINE=99413670; PubMed=10485660;  
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,

RA Sung Y.C., Oh B.-H.;  
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with  
 RT selective antitumor activity."  
 RL Immunity 11:253-261(1999).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,  
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and  
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity  
 CC may be modulated by binding to the decoy receptors  
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot  
 CC induce apoptosis.  
 CC -!- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per  
 CC trimer.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG  
 CC AND PROSTATE.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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 CC -----

DR EMBL; U37518; AAC50332.1; -.  
 DR EMBL; U57059; AAB01233.1; -.  
 DR EMBL; BC032722; AAH32722.1; -.  
 DR PDB; 1D0G; 22-OCT-99.  
 DR PDB; 1D4V; 01-NOV-99.  
 DR PDB; 1D2Q; 11-FEB-00.  
 DR PDB; 1DG6; 26-SEP-01.  
 DR Genew; HGNC:11925; TNFSF10.  
 DR MIM; 603598; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0005102; F:receptor binding; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS0049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;  
 KW Zinc; 3D-structure.  
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).  
 FT METAL 230 230 ZINC.  
 FT STRAND 123 127

FT	TURN	130	131
FT	TURN	137	139
FT	STRAND	149	150
FT	STRAND	163	165
FT	STRAND	167	170
FT	TURN	171	172
FT	STRAND	173	176
FT	STRAND	180	193
FT	STRAND	205	213
FT	STRAND	220	228
FT	STRAND	237	250
FT	TURN	252	253
FT	STRAND	255	260
FT	HELIX	263	265
FT	STRAND	266	267
FT	TURN	270	272
FT	STRAND	274	281
SQ	SEQUENCE	281 AA;	32509 MW; DDAAAF78DAAB2F6D CRC64;

Query Match 14.9%; Score 251.5; DB 1; Length 281;  
 Best Local Similarity 24.1%; Pred. No. 2.3e-14;  
 Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

Qy	42	PAASRSMFVALLGLGLGQVVC	SVALFFYFRAQMD--PNRI	SEDGTHCIYRILRLHENADF	99
		: :: : ::	:  :    ::	::   :	:
Db	10	PSLGQTCVLIVIFTVLLQSLC	VAVTYVYFTNELKQM	QDKYSKSGIACF-----	LKED--- 61
Qy	100	QDTTLESQDTKLIPDSCRRIK	QAFQGA	VQKELQHIVGSQHIRAEKAM	VDGSWLDLAKRSK 159
		: :   : :	::	:  : :  :  : :	: :
Db	62	-DSYWDPNDEESMNSPCWQVKW	-----	QLRQLVRKMILRTSEETI	-----STVQEQK 107
Qy	160	LEAQPF-----	AHLT-----	INATDIPSGSHKVSL----	SSWYHDR-GWAKISNM 199
			:	: : :  :	: :  :
Db	108	QNISPLVRERGPQRVA	AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRS	GHSLNL	167
Qy	200	TFSNGKLIVNQDGFYYLYANIC	FRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG	259	
		: :::    : :	:	: :  :  :	
Db	168	HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQM	VQYIYKYT-SYPDPILLM	KSA	226
Qy	260	STKYWSGNSEFHFYSINVG	GFFKLRS	GEEISIEVSNPSLLDPDQDATYFGAFKV	313
		:: :         : :	:   : :	:    : :	
Db	227	RNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV	280		

# RESULT 5

TN10\_MOUSE

ID	TN10_MOUSE	STANDARD;	PRT;	291 AA.
AC	P50592;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related			
DE	apoptosis inducing ligand) (TRAIL protein).			
GN	TNFSF10 OR TRAIL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96111955; PubMed=8777713;  
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,  
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,  
 RA Goodwin R.G.;  
 RT "Identification and characterization of a new member of the TNF  
 RT family that induces apoptosis.";  
 RL Immunity 3:673-682(1995).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,  
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and  
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity  
 CC may be modulated by binding to the decoy receptors  
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot  
 CC induce apoptosis.  
 CC -!- SUBUNIT: Homotrimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: WIDESPREAD.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 DR EMBL; U37522; AAC52345.1; -.  
 DR HSSP; P50591; 1D0G.  
 DR MGD; MGI:107414; Tnfsf10.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.  
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;  
  
 Query Match 14.7%; Score 248; DB 1; Length 291;  
 Best Local Similarity 25.4%; Pred. No. 4.9e-14;  
 Matches 79; Conservative 52; Mismatches 100; Indels 80; Gaps 13;  
  
 Qy 46 RSMFVALLGLG-LGQVVCVSLFFYFRAQMD--PNRISEDGTHCIYRIILRLHENADFQDT 102  
 | | : : : | | | : | | : | : | | : : | | :  
 Db 17 RMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK-----TDEDFWDS 71  
  
 Qy 103 TLESQDTKLIPDSCRRIK-----QAFQ-----GAVQKEL 131



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      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      72 T----DGEILNRPCLOVKRQLYQLIEEVTLRFTQDTISTVPEKQLSTPPLPRGGRPKVA 127

Qy      132 QHIVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDR 191
      || |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      128 AHITGITR-RSNSALI-----PISKDGKTLGQ-----KIESWESSR 162

Qy      192 -GWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYL-----QLMVYV 242
      | : : : : | | : : : | : | : : | | |   |   |   |   |   |   |
Db      163 KGHSFLNHVLFNRNGELVIEQEGLYIYSQTYFRFQEAED--ASKMVSKDKVRTKQLVQYI 220

Qy      243 TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFKLRSGEIEISIEVSNPSLLDPD 302
      | :   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      221 YKYT-SYPDPIVLMKSARNSCWSRDAEYGLYSIQGGLFELKKNDRI FVSVTNEHLMDDL 279

Qy      303 QDATYFGAFKV 313
      | : : : | : : : :
Db      280 QEASFFGAFLI 290

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RESULT 6

TNF6\_PIG

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ID      TNF6_PIG          STANDARD;          PRT;    282 AA.
AC      Q9BEA8; Q95M04; Q95N10;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE      ligand).
GN      TNFSF6 OR FASL.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21322533; PubMed=11429161;
RA      Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
RT      "Molecular cloning, characterization, and expression of porcine Fas
RT      ligand (CD95 ligand).";
RL      J. Interferon Cytokine Res. 21:305-312(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Guanxi bama miniature pig;
RA      Zhu N., Young Y.;
RT      "Molecular cloning and characterization of porcine Fas ligand cDNA.";
RL      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lymphoid;
RA      Tsuyuki S., Kono M., Bloom E.T.;
RT      "Cloning and potential utility of porcine Fas ligand: overexpression
RT      in porcine cells protects them from attack by human cytolytic cells.";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Landrace x Large Yorkshire white; TISSUE=Thymocytes;

```

RX MEDLINE=21653191; PubMed=11792426;  
 RA Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;  
 RT "Porcine Fas-ligand gene: genomic sequence analysis and comparison  
 RT with human gene.";  
 RL Mol. Immunol. 38:581-586(2002).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- INDUCTION: By IL-18.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 DR EMBL; AB027297; BAB40919.1; -.  
 DR EMBL; AY033634; AAK56449.1; -.  
 DR EMBL; AF397407; AAK84408.1; -.  
 DR EMBL; AB069764; BAB64291.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 FT CHAIN 1 282 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, MEMBRANE FORM.  
 FT CHAIN 131 282 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).  
 FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 104 282 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 4 70 PRO-RICH.  
 FT DOMAIN 45 56 POLY-PRO.  
 FT SITE 130 131 CLEAVAGE (BY SIMILARITY).

FT DISULFID 203 234 POTENTIAL.  
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 5 5 F -> L (IN REF. 4).  
 FT CONFLICT 57 57 T -> P (IN REF. 2).  
 SQ SEQUENCE 282 AA; 31756 MW; 6743DAA1145671FB CRC64;

Query Match 11.9%; Score 200; DB 1; Length 282;  
 Best Local Similarity 23.0%; Pred. No. 6.5e-10;  
 Matches 76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;

Qy 22 PGAPHEGPLHAPPPAPHQPPAA---SRSM-----FVA 51  
 || | | ||| | || : ||  
 Db 37 PGRP--GQRRPPPPPPPPPPPTLLPSRPLPLPPPSLKKKRDHNAGLCLLMFFMVLVA 94  
 Qy 52 LLGLGLGQVVC SVALFFYFRAQMDPNRI SEDGTHCIYRILRLHENADFQDTTLESQDTKL 111  
 |:|||| :| | : : | |:| : |  
 Db 95 LVGLGLG-----MFQLFHLQKE-----LTELRRESASQRHT----- 124  
 Qy 112 IPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHT-- 169  
 : |: :| :: :|| | : ||||  
 Db 125 -----ESSLEKQIGHPNLPSEKK-----ELRKVAHLTGK 153  
 Qy 170 INATDIPSGSHKVSLSWYHDRGWAKISNMTFSNGKLIQVNDGFYYLYANICFRHHETSG 229  
 |: || | | :| : : | |:| | |:|: : || :  
 Db 154 PNSRSIP-----LEWEDTYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGQYCN- 204  
 Qy 230 DLATEYLQIMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGF FKL 283  
 : | || |: | : | ||:| | : :| :| ||  
 Db 205 ---NQPLSHKVY-TRNS-RYPQDLVLMEGKMMNYCTTGQMWARSS-----YLGAVFNL 252  
 Qy 284 RSCEEISIEVSNPSLLDPDQDATYFGAFKV 313  
 | : : : || ||:: : : |:|| :|:  
 Db 253 TSADHLYVNVSELSLVNFEESKTFFGLYKL 282

# RESULT 7

## TNF6\_HUMAN

ID TNF6\_HUMAN STANDARD; PRT; 281 AA.  
 AC P48023; Q9BZP9;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)  
 DE (Apoptosis antigen ligand) (APTL) (CD178 antigen).  
 GN TNFSF6 OR FASL OR APT1LG1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=95105731; PubMed=7528780;  
 RA Alderson M.;  
 RT "Fas ligand mediates activation-induced cell death in human T  
 lymphocytes.";

RL J. Exp. Med. 181:71-77(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=95127560; PubMed=7826947;  
 RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;  
 RT "Human Fas ligand: gene structure, chromosomal location and species  
 RT specificity.";  
 RL Int. Immunol. 6:1567-1574(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=95071350; PubMed=7980502;  
 RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,  
 RA Fusamoto H., Kamada T.;  
 RT "Role of Fas ligand in apoptosis induced by hepatitis C virus  
 RT infection.";  
 RL Biochem. Biophys. Res. Commun. 204:468-474(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Leukocyte;  
 RA Zeytun A., Nagarkatti M., Nagarkatti P.S.;  
 RT "Isolation and characterization of a new naturally occurring variant of  
 RT human Fas ligand that is expressed only in membrane bound form.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Wilkinson J.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Blood;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP SEQUENCE OF 1-10 FROM N.A.

RC TISSUE=Blood;  
 RA Matsumura M., Nakanishi Y., Ohba Y.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.  
 RX MEDLINE=97373583; PubMed=9228058;  
 RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,  
 RA Terskikh A., Peitsch M.C., Tschopp J.;  
 RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";  
 RL J. Biol. Chem. 272:18827-18833(1997).  
 RN [10]  
 RP PROCESSING.  
 RX MEDLINE=98087475; PubMed=9427603;  
 RA Tanaka M., Itai T., Adachi M., Nagata S.;  
 RT "Downregulation of Fas ligand by shedding.";  
 RL Nat. Med. 4:31-36(1998).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects.  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. May be released  
 CC into the extracellular fluid, probably by cleavage from the cell  
 CC surface.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=P48023-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P48023-2; Sequence=VSP\_006443, VSP\_006444;  
 CC -!- PTM: N-glycosylated.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing.  
 CC -!- DISEASE: Defects in TNFSF6 are a cause of autoimmune  
 CC lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as  
 CC Canale-Smith syndrome (CSS). ALPS is a childhood syndrome  
 CC involving hemolytic anemia and thrombocytopenia with massive  
 CC lymphadenopathy and splenomegaly.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/333879674\_g.htm".  
 CC -----  
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 CC -----  
 DR EMBL; X89102; CAA61474.1; -.  
 DR EMBL; U08137; AAC50071.1; -.  
 DR EMBL; U11821; AAC50124.1; -.  
 DR EMBL; D38122; BAA07320.1; -.

DR EMBL; AF288573; AAG60017.1; -.  
 DR EMBL; Z96050; CAB09424.1; -.  
 DR EMBL; BC017502; AAH17502.1; -.  
 DR EMBL; AB013303; BAA32542.1; -.  
 DR PIR; I38707; I38707.  
 DR HSSP; P01375; 1TNF.  
 DR Genew; HGNC:11936; TNFSF6.  
 DR MIM; 134638; -.  
 DR MIM; 601859; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005102; F:receptor binding; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;  
 KW Alternative splicing; Antigen.  
 FT CHAIN 1 281 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, MEMBRANE FORM.  
 FT CHAIN 130 281 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, SOLUBLE FORM.  
 FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 103 281 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 4 70 PRO-RICH.  
 FT DOMAIN 45 65 POLY-PRO.  
 FT SITE 129 130 CLEAVAGE.  
 FT DISULFID 202 233 POTENTIAL.  
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 117 127 STSQMHTASSL -> ATPVHPLKKRS (in isoform  
 FT 2).  
 FT /FTId=VSP\_006443.  
 FT VARSPLIC 128 281 Missing (in isoform 2).  
 FT /FTId=VSP\_006444.  
 FT MUTAGEN 206 206 P->D,F,R: LOWERS BINDING TO TNFRSF6 AND  
 FT REDUCES CYTOTOXICITY MORE THAN 100-FOLD.  
 FT MUTAGEN 218 218 Y->F,R: LOWERS BINDING TO TNFRSF6 AND  
 FT ABOLISHES CYTOTOXICITY.  
 FT MUTAGEN 275 275 F->L: ABOLISHES BINDING TO TNFRSF6 AND  
 FT CYTOTOXICITY.  
 SQ SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;

Query Match 11.2%; Score 189; DB 1; Length 281;

Best Local Similarity 21.7%; Pred. No. 5.8e-09;  
Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;

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QY      22 PGAPHEGPHLHAPPPAP----HQPPAASRS-----MFVALLGLGLGQVVCS 63
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Db      46 P P P P P P P L P P P P P P P L P P L P L P L K R G N H S T G L C L L V M F F M V L V A L V G L G L G ----- 100

QY      64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF 123
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     101 --MFQLFHLQ-----KELAE LRESTSQMHTA----- 124

QY     124 QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFALHT--INATDIPSGSHK 181
      : : : | : | | | | | | | | | | | | | | | | | | | | | |
Db     125 -SSLEKQIGH-----PSPPEKKE L R K V A H L T G K S N S R S M P ----- 159

QY     182 VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIMVY 241
      | | | | | : | : : | | : : : | | : : : | | : | | | | | |
Db     160 ---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----LPLSHK 210

QY     242 VTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFKLRSGEESIEVSN 295
      | : | | | : | : | | | : | : | | | : | | | | : : : | |
Db     211 VYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSS-----YLGAVFNLT SADHLYVN VSE 263

QY     296 PSLLDPDQDATYFGAFKV 313
      | | : : : | : | | : | :
Db     264 LSLVNFEESQTFFGLYKL 281

```

# RESULT 8

## TNF6\_MACMU

```

ID      TNF6_MACMU      STANDARD;      PRT;      280 AA.
AC      Q9MYL6; Q9BDM5;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE      (CD95L protein).
GN      TNFSF6 OR FASL OR CD95L.
OS      Macaca mulatta (Rhesus macaque),
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS      Macaca nemestrina (Pig-tailed macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9544, 9541, 9545;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      SPECIES=M.mulatta; TISSUE=Lymphocytes;
RX      MEDLINE=21383618; PubMed=11491535;
RA      Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA      Weiss W.R., Ansari A.A.;
RT      "Cloning, sequencing, and homology analysis of nonhuman primate
RT      Fas/Fas-ligand and co-stimulatory molecules.";
RL      Immunogenetics 53:315-328(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;

```

RA Kirii Y., Inoue T., Yoshino K.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 DR EMBL; AF344856; AAK37539.1; -.  
 DR EMBL; AB035138; BAA90294.1; -.  
 DR EMBL; AB035139; BAA90295.1; -.  
 DR EMBL; AB035140; BAA90296.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, MEMBRANE FORM.  
 FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).  
 FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 102 280 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 4 69 PRO-RICH.  
 FT DOMAIN 45 64 POLY-PRO.  
 FT SITE 128 129 CLEAVAGE (BY SIMILARITY).  
 FT DISULFID 201 232 POTENTIAL.  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).



FT CONFLICT 60 60 S -> P (IN REF. 1).  
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

QY	22	PGAPHEGPLHAPPPAP-----HQPPAASRS-----MFVALLGLGLGQVVCS	63
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Db	45	PPPPPPPPPLPPPPPSPLPPLPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLG----	99
QY	64	VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF	123
		:          : ::  :	
Db	100	--MFQLFHLQ-----KELAELESTSQKHTA-----	123
QY	124	QGAVQKELQHIVGSQHIRAEKAMVDGSWLDIAKRSKLEAQPFALHT--INATDIPSGSHK	181
		::: ::      :        : :	
Db	124	--SSLEKQIGH-----PSPPEKEKQRKVAHLTGKPNSRSM-----	158
QY	182	VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFFYYLYANICFRHHETSGDLATEYLQLMVY	241
		: :   : : :   : : : :	
Db	159	---LEWEDTYGIVLLSGVKYKKGLVINETGLYFVYSKVYFR----GQSCTN-LPLSHK	209
QY	242	VTKTSIKIPSSHITLMKGGSTKYWSGNSEFHFY SINVGGF FKLRS GEEI SIEVS NP SLLDP	301
		:     :  :    : :   :       : : :      ::	
Db	210	VYMRNSKYPQDLVMMEGKMMSYCT-TGQMWAHSSYLGA VFNLT SADHLYVNVS ELSLVNF	268
QY	302	DQDATYFGAFKV	313
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Db	269	EESOTFFGLYKL	280

## TNF6 MOUSE

RX MEDLINE=95388076; PubMed=7544870;  
 RA Peitsch M.J., Tschopp J.J.;  
 RT "Comparative molecular modelling of the Fas-ligand and other members  
 RT of the TNF family.";  
 RL Mol. Immunol. 32:761-772(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL).  
 RX MEDLINE=95196085; PubMed=7889405;  
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
 RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a  
 RT TNF family gene cluster.";  
 RL Immunity 1:131-136(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL).  
 RC STRAIN=BALB/c;  
 RA Fenner M.H., Shioda T., Isselbacher K.J.;  
 RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in  
 RT two amino acids.";  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM FASLS).  
 RC STRAIN=C3H; TISSUE=Spleen;  
 RX MEDLINE=20021694; PubMed=10552956;  
 RA Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,  
 RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;  
 RT "Cloning and expression of a short Fas ligand: A new alternatively  
 RT spliced product of the mouse Fas ligand gene.";  
 RL Blood 94:3456-3467(1999).  
 RN [6]  
 RP CHARACTERIZATION OF VARIANT GLD.  
 RX MEDLINE=96091792; PubMed=7495745;  
 RA Hahne M., Peitsch M.C., Irmeler M., Schroeter M., Lowin B.,  
 RA Rousseau M., Bron C., Renno T., French L., Tschopp J.;  
 RT "Characterization of the non-functional Fas ligand of gld mice.";  
 RL Int. Immunol. 7:1381-1386(1995).  
 RN [7]  
 RP VARIANTS ALA-184 AND GLY-218.  
 RC STRAIN=C57BL/6, C3H, MRL, SJL, NOD, NZB, NZW, BALB/c, DBA/1, and  
 RC DBA/2;  
 RX MEDLINE=97268671; PubMed=9108079;  
 RA Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,  
 RA Yagita H.;  
 RT "Polymorphism of murine Fas ligand that affects the biological  
 RT activity.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);  
 CC Secreted (isoforms FASL and FASLS).  
 CC -!- ALTERNATIVE PRODUCTS:

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CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=FasL;
CC      IsoId=P41047-1; Sequence=Displayed;
CC      Name=FasLS;
CC      IsoId=P41047-2; Sequence=VSP_006445;
CC      -!- PTM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -!- DISEASE: A deficiency in this protein is the cause of generalized
CC      lymphoproliferation disease phenotype (gld). Gld mice present
CC      lymphadenopathy and autoantibody production. The phenotype is
CC      recessively inherited.
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U06948; AAA17800.1; -.
DR      EMBL; U10984; AAA19778.1; -.
DR      EMBL; S76752; AAB33780.1; -.
DR      EMBL; U58995; AAB02915.1; -.
DR      EMBL; AF119335; AAD52106.1; -.
DR      PIR; A53062; A53062.
DR      HSSP; P01375; 4TSV.
DR      MGD; MGI:99255; Tnfsf6.
DR      InterPro; IPR008064; Fas_ligand.
DR      InterPro; IPR006053; TNF_abc.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR008983; TNF_like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      PRINTS; PR01681; FASLIGAND.
DR      PRINTS; PR01234; TNECROSISFCT.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; 1.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
KW      Disease mutation; Polymorphism; Alternative splicing.
FT      CHAIN      1      279      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 6, MEMBRANE FORM.
FT      CHAIN      128      279      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT      DOMAIN      1      78      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      79      100      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                     (POTENTIAL).
FT      DOMAIN      101      279      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN      4      69      PRO-RICH.
FT      DOMAIN      45      51      POLY-PRO.
FT      SITE      127      128      CLEAVAGE (BY SIMILARITY).
FT      DISULFID      200      231      POTENTIAL.
FT      CARBOHYD      117      117      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      182      182      N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 210 Missing (in isoform FasLS).  
 FT /FTid=VSP\_006445.  
 FT VARIANT 184 184 T -> A (IN STRAINS BALB/C AND DBA;  
 FT ENHANCES CYTOTOXICITY).  
 FT VARIANT 218 218 E -> G (IN STRAINS BALB/C AND DBA;  
 FT ENHANCES CYTOTOXICITY).  
 FT VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL  
 FT TO ITS RECEPTOR).  
 SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;

Query Match 10.9%; Score 184.5; DB 1; Length 279;  
 Best Local Similarity 21.7%; Pred. No. 1.4e-08;  
 Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;

QY 13 RGSEEMGGGPGAPHEGPLHAPPPAPHQP-----PAASRSMFVALLGLGL 57  
 || :: | | || | | | | : |||::||  
 Db 38 RGPDQRRPPPPPPVSPPLPPPSQPLPLPLPLPLKKKDHNTNLWLPVVFVFMVLVALVGMGL 97  
 QY 58 GQVVCVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117  
 | :|:: |  
 Db 98 G-----MYQLFHL----- 105  
 QY 118 RIKQAFQGA VQKELQHI--VGSQHRA---EKAMVDGSWLDLAKRSKLEAQPF AHLTINA 172  
 ||| : :| :: || : : | | : ||| |  
 Db 106 -----QKELAE LREFTNQSLKVSSF EKQIANPS----TPSEKKEPRSV AHLTGN- 150  
 QY 173 TDIPSGSHKVSLS-SWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231  
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 Db 151 -----PHSRSI PLEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN--- 201  
 QY 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVG GFFKLRSGEEISI 291  
 : | ||: : | | ||: | : : | : | | | : : :  
 Db 202 -NQPLNHKVYMRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSYLGA VFNLT SADHLYV 257  
 QY 292 EVSNPSLLDPDQDATYFGAFKV 313  
 :| ||:: :: |:|| :|:  
 Db 258 NISQLSLINFEEKSTFFGLYKL 279

# RESULT 10

TNF6\_CERTO

ID TNF6\_CERTO STANDARD; PRT; 280 AA.

AC Q9BDN1;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)  
 DE (CD95L protein).

GN TNFSF6 OR FASL OR CD95L.

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Cercopithecus.

OX NCBI\_TaxID=9531;

RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphocytes;  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 RT Fas/Fas-ligand and co-stimulatory molecules.";  
 RL Immunogenetics 53:315-328(2001).  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that  
 CC transduces the apoptotic signal into cells. May be involved in  
 CC cytotoxic T cell mediated apoptosis and in T cell development.  
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of  
 CC peripheral tolerance, in the antigen-stimulated suicide of mature  
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3  
 CC modulates its effects (By similarity).  
 CC -!- SUBUNIT: Homotrimer (Probable).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By  
 CC similarity).  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 DR EMBL; AF344847; AAK37606.1; -.  
 DR HSSP; P01375; 4TSV.  
 DR InterPro; IPR008064; Fas\_ligand.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01681; FASLIGAND.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR ProDom; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.  
 FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, MEMBRANE FORM.  
 FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY  
 FT MEMBER 6, SOLUBLE FORM (BY SIMILARITY).  
 FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 102 280 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 4 69 PRO-RICH.  
 FT DOMAIN 45 64 POLY-PRO.  
 FT SITE 128 129 CLEAVAGE (BY SIMILARITY).  
 FT DISULFID 201 232 POTENTIAL.

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 10.8%; Score 182.5; DB 1; Length 280;  
 Best Local Similarity 22.4%; Pred. No. 2.1e-08;  
 Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

QY 22 PGAPHEGPLHAPPPAPHQPP-----AASRS-----MFVALLGLGLGQVVC 62  
 | | | | | | | | : | : | | | | |  
 Db 46 PPPPPPPPL--PPPPPPPLPPLPLPPLKKRGNHSTGLCLLMFFMVLVALVGLGLG---- 99  
 QY 63 SVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQA 122  
 : | | | | | | | : : : : :  
 Db 100 ---MFQLFHLQ-----KELAELESTSQKHTA----- 123  
 QY 123 FQGAVQKELQHIVGSQHIRAEKAMVDGSWDLAKRSKLEAQPFAHLT--INATDIPSGSH 180  
 : : : : | | : | | | | : : |  
 Db 124 --SSLEKQIGH-----PSPPEKKEQRKVAHLTGKPNRSRSM----- 158  
 QY 181 KVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYLYANICFRHHETSGDLATEYLQLMV 240  
 | | : | : : | | : : | | : : | | | |  
 Db 159 ----LEWEDTYGIVLLSGVKYKGGVLINETGLYFVYSKVYFR-----GQSCTN-LPLSH 208  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFKLRSGEESIEVSNPSLLD 300  
 | : | | : : | : : : | | | : : : | | : :  
 Db 209 KVMRNSKYPQDLVMEGKMSYCT-TGQMAHSSYLGAVENTLSTDHLYNVNSELVLN 267  
 QY 301 PDQDATYFGAFKV 313  
 : : | : | : :  
 Db 268 FEESQTFFGLYKL 280

# RESULT 11

## TNF5\_BOVIN

ID TNF5\_BOVIN STANDARD; PRT; 261 AA.  
 AC P51749;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-  
 DE related activation protein) (TRAP) (T cell antigen GP39).  
 GN TNFSF5 OR CD40LG OR CD40L.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=96006582; PubMed=7590981;  
 RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;  
 RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand  
 RT and tumor necrosis factor alpha."  
 RL Immunogenetics 42:430-431(1995).

CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell  
CC proliferation in the absence of co-stimulus as well as IgE  
CC production in the presence of IL-4. Involved in immunoglobulin  
CC class switching (By similarity).  
CC -!- SUBUNIT: Homotrimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
CC extracellular soluble form (By similarity).  
CC -!- PTM: The soluble form derives from the membrane form by  
CC proteolytic processing (By similarity).  
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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DR EMBL; Z48469; CAA88363.1; -.  
DR PIR; S53090; S53090.  
DR HSSP; P29965; 1ALY.  
DR GO; GO:0016021; C:integral to membrane; ISS.  
DR GO; GO:0005174; F:CD40 receptor binding; ISS.  
DR GO; GO:0042100; P:B-cell proliferation; ISS.  
DR GO; GO:0006954; P:inflammatory response; ISS.  
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.  
DR GO; GO:0030168; P:platelet activation; ISS.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR006052; TNF\_family.  
DR InterPro; IPR008983; TNF\_like.  
DR InterPro; IPR003636; TNF\_subf.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01702; CD40LIGAND.  
DR ProDom; PD008600; TNF\_5; 1.  
DR ProDom; PD002012; TNF\_subf; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

FT	CHAIN	1	261	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 5, MEMBRANE FORM.
FT	CHAIN	113	261	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
FT	DOMAIN	1	22	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	23	46	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT				(POTENTIAL).
FT	DOMAIN	47	261	EXTRACELLULAR (POTENTIAL).
FT	SITE	112	113	CLEAVAGE (BY SIMILARITY).
FT	DISULFID	178	218	POTENTIAL.
FT	CARBOHYD	240	240	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	261 AA;	29242 MW;	8491FEFB30A787FD CRC64;

Query Match 10.5%; Score 176.5; DB 1; Length 261;  
Best Local Similarity 24.2%; Pred. No. 6.3e-08;  
Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;





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CC      proteolytic processing (By similarity).
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U03470; AAC52129.1; -.
DR      PIR; A49266; A49266.
DR      HSSP; P01375; 4TSV.
DR      InterPro; IPR008064; Fas_ligand.
DR      InterPro; IPR006053; TNF_abc.
DR      InterPro; IPR006052; TNF_family.
DR      InterPro; IPR008983; TNF_like.
DR      InterPro; IPR003636; TNF_subf.
DR      Pfam; PF00229; TNF; 1.
DR      PRINTS; PR01681; FASLIGAND.
DR      PRINTS; PR01234; TNECROSISFCT.
DR      ProDom; PD002012; TNF_subf; 1.
DR      SMART; SM00207; TNF; 1.
DR      PROSITE; PS00251; TNF_1; 1.
DR      PROSITE; PS50049; TNF_2; 1.
KW      Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT      CHAIN          1      278      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 6, MEMBRANE FORM.
FT      CHAIN          127     278      TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT                                     MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT      DOMAIN         1       77      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM       78      99      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                     (POTENTIAL).
FT      DOMAIN        100     278      EXTRACELLULAR (POTENTIAL).
FT      DOMAIN         4       69      PRO-RICH.
FT      DOMAIN        45      58      POLY-PRO.
FT      SITE          126     127      CLEAVAGE (BY SIMILARITY).
FT      DISULFID       199     230      POTENTIAL.
FT      CARBOHYD       116     116      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD       247     247      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD       257     257      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;

Query Match          10.4%; Score 175.5; DB 1; Length 278;
Best Local Similarity 20.3%; Pred. No. 8.4e-08;
Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

Qy      21 GPGAPHEGPLHAPPPAPHPQPPAASRSM-----FVALLGLGL 57
      ||| | |||:| ||: : |||:|:|
Db      39 GPGQRRPPP--PPPPPSPLPPPSQPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGL 96

Qy      58 GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117
      | : | | : | | : | : | : | : | : :
Db      97 G-----MYQLFHLQKELAELEFTNHSI-RVSSFQKQIANPSTPSETKKPRSV----- 143

Qy      118 RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPF AHLTINATDIPS 177

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Db      144 -----| | | | |-----AHLTGNPR----- 151
Qy      178 GSHKVSLSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ 237
      | : | | | | | : : | : : | : : | : : | : : |
Db      152 -SRSIPL-EWEDTYGTALISGVKYKGGGLVINEAGLYFVYSKVYFRGQSCN----SQPLS 205
Qy      238 LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEIEISIEVSNPS 297
      ||: : | | | | : : | : : | : | | | : : : | |
Db      206 HKVYM--RNFKYPGDLVLMEEKKLNCT-TGQIAHSSYLGAVFNLTVADHLYVNISQLS 262
Qy      298 LLDPDQDATYFGAFKV 313
      | : : : | : | | : | :
Db      263 LINFEESKTFFGLYKL 278

```

# RESULT 13

## TNF5\_CALJA

```

ID      TNF5_CALJA      STANDARD;      PRT;      261 AA.
AC      Q9BDN3;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE      L) (CD154 protein).
GN      TNFSF5 OR CD40LG OR CD40L.
OS      Callithrix jacchus (Common marmoset).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC      Callithrix.
OX      NCBI_TaxID=9483;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lymphocytes;
RX      MEDLINE=21383618; PubMed=11491535;
RA      Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA      Weiss W.R., Ansari A.A.;
RT      "Cloning, sequencing, and homology analysis of nonhuman primate
RT      Fas/Fas-ligand and co-stimulatory molecules.";
RL      Immunogenetics 53:315-328(2001).
CC      -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC      proliferation in the absence of co-stimulus as well as IgE
CC      production in the presence of IL-4. Involved in immunoglobulin
CC      class switching (By similarity).
CC      -!- SUBUNIT: Homotrimer (By similarity).
CC      -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC      extracellular soluble form (By similarity).
CC      -!- PTM: The soluble form derives from the membrane form by
CC      proteolytic processing (By similarity).
CC      -!- SIMILARITY: Belongs to the tumor necrosis factor family.

```

```

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DR EMBL; AF344844; AAK37603.1; -.

DR HSSP; P29965; 1ALY.

DR GO; GO:0016021; C:integral to membrane; ISS.

DR GO; GO:0005174; F:CD40 receptor binding; ISS.

DR GO; GO:0042100; P:B-cell proliferation; ISS.

DR GO; GO:0006954; P:inflammatory response; ISS.

DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.

DR GO; GO:0030168; P:platelet activation; ISS.

DR InterPro; IPR003263; TNF\_5.

DR InterPro; IPR006052; TNF\_family.

DR InterPro; IPR008983; TNF\_like.

DR InterPro; IPR003636; TNF\_subf.

DR Pfam; PF00229; TNF; 1.

DR PRINTS; PR01702; CD40LIGAND.

DR ProDom; PD008600; TNF\_5; 1.

DR ProDom; PD002012; TNF\_subf; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00251; TNF\_1; 1.

DR PROSITE; PS50049; TNF\_2; 1.

KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

FT	CHAIN	1	261	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 5, MEMBRANE FORM.
FT	CHAIN	113	261	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT				MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
FT	DOMAIN	1	22	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	23	43	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT				(POTENTIAL).
FT	DOMAIN	44	261	EXTRACELLULAR (POTENTIAL).
FT	SITE	112	113	CLEAVAGE (BY SIMILARITY).
FT	DISULFID	178	218	POTENTIAL.
FT	CARBOHYD	240	240	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	261 AA;	29360 MW;	10CA588D923754EB CRC64;

Query Match 10.1%; Score 169.5; DB 1; Length 261;

Best Local Similarity 24.6%; Pred. No. 2.5e-07;

Matches 71; Conservative 55; Mismatches 120; Indels 43; Gaps 15;

Qy	33	PPPPAPHQPPAASRSMFVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL	91
Db	8	PVPSAATGPPVSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDE-----R	57
Qy	92	RLHENADFQDT--TLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG	149
Db	58	NLHEDFVFMKTIQRCNTGERSLSLLNCEEIKSQFEGFV-KDIM-----LNKEEKKKEN	109
Qy	150	SWLDLAKRSKLEAQPPFAHLTINATDIPSGSHKVSLSWYHDRGWAKISN--MTFSNGK-L	206
Db	110	SF-EMQKGDQ-NPQIAAHVISEAS-----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQL	161
Qy	207	IVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYW	264
Db	162	TVKRQGLYYIYAQVTFCSNREASSQAP-----FIASLCLKPPNRFERILLRAANTH--	212
Qy	265	SGNSEFHFYSINVGGFKKLSGEEISIEVSNPSLLDPDQDATYFGAFKV	313

## RESULT 14

## TNF5\_AOTTR

ID TNF5\_AOTTR STANDARD; PRT; 261 AA.  
AC Q9BDM3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-  
L) (CD154 protein).  
GN TNFSF5 OR CD40LG OR CD40L.  
OS Aotus trivirgatus (Night monkey) (Douroucoulis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.  
OX NCBI\_TaxID=9505;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphocytes;  
RX MEDLINE=21383618; PubMed=11491535;  
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
RA Weiss W.R., Ansari A.A.;  
RT "Cloning, sequencing, and homology analysis of nonhuman primate  
RT Fas/Fas-ligand and co-stimulatory molecules."  
RL Immunogenetics 53:315-328(2001).  
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell  
CC proliferation in the absence of co-stimulus as well as IgE  
CC production in the presence of IL-4. Involved in immunoglobulin  
CC class switching (By similarity).  
CC -!- SUBUNIT: Homotrimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
CC extracellular soluble form (By similarity).  
CC -!- PTM: The soluble form derives from the membrane form by  
CC proteolytic processing (By similarity).  
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
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-----  
DR EMBL; AF344860; AAK37542.1; -.  
DR HSSP; P29965; 1ALY.  
DR GO; GO:0016021; C:integral to membrane; ISS.  
DR GO; GO:0005174; F:CD40 receptor binding; ISS.  
DR GO; GO:0042100; P:B-cell proliferation; ISS.  
DR GO; GO:0006954; P:inflammatory response; ISS.  
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.  
DR GO; GO:0030168; P:platelet activation; ISS.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR006052; TNF\_family.  
DR InterPro; IPR008983; TNF\_like.  
DR InterPro; IPR003636; TNF\_subf.



OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93076854; PubMed=1280226;  
 RA Graf D., Korthaeuer U., Mages H.W., Senger G., Kroccek R.A.;  
 RT "Cloning of TRAP, a ligand for CD40 on human T cells.";  
 RL Eur. J. Immunol. 22:3191-3194(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93049181; PubMed=1385114;  
 RA Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,  
 RA Braesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,  
 RA Aruffo A.;  
 RT "The human T cell antigen gp39, a member of the TNF gene family, is a  
 RT ligand for the CD40 receptor: expression of a soluble form of gp39  
 RT with B cell co-stimulatory activity.";  
 RL EMBO J. 11:4313-4321(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235.  
 RX MEDLINE=93145330; PubMed=7678782;  
 RA Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatovich A.,  
 RA Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer M.,  
 RA Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.;  
 RT "The CD40 ligand, gp39, is defective in activated T cells from  
 RT patients with X-linked hyper-IgM syndrome.";  
 RL Cell 72:291-300(1993).  
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 CC -!- FUNCTION: Mediates B-cell proliferation in the absence of co-  
 CC stimulus as well as IgE production in the presence of IL-4.  
 CC Involved in immunoglobulin class switching.  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form.  
 CC -!- TISSUE SPECIFICITY: Specifically expressed on activated CD4+  
 CC T-lymphocytes.  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing.  
 CC -!- DISEASE: Defects in TNFSF5 are the cause of X-linked  
 CC immunodeficiency with hyper-IgM type 1 (HIGM1) [MIM:308230]. HIGM1  
 CC is an immunoglobulin isotype switch defect characterized by  
 CC elevated concentrations of serum IgM and decreased amounts of all  
 CC other isotypes. Affected males present at an early age (usually  
 CC within the first year of life) recurrent bacterial and  
 CC opportunistic infections, including pneumocystis carinii pneumonia  
 CC and intractable diarrhea due to cryptosporidium infection. Despite  
 CC substitution treatment with intravenous immunoglobulin, the  
 CC overall prognosis is rather poor, with a death rate of about 10%  
 CC before adolescence.  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -!- DATABASE: NAME=CD40Lbase;  
 CC NOTE=European CD40L defect database (mutation db);  
 CC WWW="http://www.expasy.org/cd40lbase/";  
 CC FTP="ftp://ftp.expasy.org/databases/cd40lbase".  
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD154 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd154.htm".

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DR EMBL; X68550; CAA48554.1; -.  
 DR EMBL; Z15017; CAA78737.1; -.  
 DR EMBL; X67878; CAA48077.1; -.  
 DR EMBL; L07414; AAA35662.1; -.  
 DR EMBL; D31797; BAA06599.1; -.  
 DR EMBL; D31793; BAA06599.1; JOINED.  
 DR EMBL; D31794; BAA06599.1; JOINED.  
 DR EMBL; D31795; BAA06599.1; JOINED.



DR EMBL; D31796; BAA06599.1; JOINED.  
 DR PIR; S28017; I53476.  
 DR PDB; 1ALY; 17-SEP-97.  
 DR PDB; 1I9R; 22-MAY-02.  
 DR Genew; HGNC:11935; TNFSF5.  
 DR MIM; 300386; -.  
 DR MIM; 308230; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0005174; F:CD40 receptor binding; IPI.  
 DR GO; GO:0006916; P:anti-apoptosis; IDA.  
 DR GO; GO:0042100; P:B-cell proliferation; IDA.  
 DR GO; GO:0006954; P:inflammatory response; IDA.  
 DR GO; GO:0045190; P:isotype switching; ISS.  
 DR GO; GO:0007159; P:leukocyte cell adhesion; NAS.  
 DR GO; GO:0030168; P:platelet activation; IDA.  
 DR GO; GO:0007165; P:signal transduction; ISS.  
 DR InterPro; IPR003263; TNF\_5.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.

Query Match 9.4%; Score 158.5; DB 1; Length 261;  
 Best Local Similarity 24.5%; Pred. No. 2.3e-06;  
 Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

Qy	45	SRSMFVALLGLGL-GQVVC	SVALFFYFRAQMDPNRI	SEDGTHCIYRILRLHENAD	FQDT-	102
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Qy	103	-TLESQDTKLIPDSC	RIKQAFQGA	VQKELQHIVGSQH	IRAEKAMVDG	SWLDLAKRSKLE 161
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Db	70	QRCNTGERSLSLLN	CEEIKSQFEGFV	-KDIM-----	LNKEETKKENSF	-EMQKGDQ-N 119
Qy	162	AQPFAHLTINATDIP	SGSHKVSLS	SWYHDRGWAKISN	--MTFSNGK-	LIVNQDGFYYLYA 218
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Db	120	PQIAAHVISEAS----	SKTTSVLQW-AE	KGYTMSNNLVT	LENGKQLTVK	RQGLYYIYA 173
Qy	219	NICFRHHETSGDL	ATEYLQIMVY	VTKTSIKIPS--	SHTLMKGGST	KYWSGNSEFHFYSIN 276
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Db	174	QVTFCSNREASSQ	AP-----	FIASLCLKSPGR	FERILLRAANTH	--SSAKPCGQQSIH 224
Qy	277	VGGFFKLRS	GEEISIEVSN	PSLLDPDQ	DATYFGAFKV	313
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Db	225	LGGVFELQPGAS	VFVNVTDPSQ	VSHGTGFTS	FGLLKL	261

Search completed: February 25, 2004, 16:29:25  
 Job time : 19 secs